

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:05:25 ; Search time 189 Seconds

(without alignments)
362.662 Million cell updates/sec

Title: US-09-770-528-2

Sequence: 1 MMVLSGALCFRMKDSALKVL.....IPEDPAMDAPITDFEQQCD 156

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseq_21:*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003s:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	819	100.0	156	2 AAW86284	Aaw86284 Rodent in
2	819	100.0	156	2 AAY28407	Aay28407 Mouse int
3	819	100.0	156	3 AAY92260	Aay92260 Murine IL
4	819	100.0	156	3 AAY45061	Aay45061 Murine TA
5	819	100.0	156	7 ABU62869	Abu62869 Mouse sec
6	819	100.0	156	8 ADJ88315	Adj88315 Mouse int
7	819	100.0	156	8 ADU04688	Adu04688 Mouse int
8	819	100.0	156	8 ADQ98213	Adq98213 Mouse TAN
9	814	99.4	155	3 AAY96937	Aay96937 Murine IL
10	814	99.4	155	4 AAB66672	Aab66672 Invention
11	814	99.4	155	4 AAB48828	Aab48828 Murine in
12	814	99.4	155	4 AAB35261	Aab35261 Murine IL
13	809	98.8	154	4 AAE06663	Aae06663 Mouse int
14	807	98.5	156	4 ADL15877	Adl15877 Human int
15	768	93.8	146	5 ABP52012	Abp52012 NOVINTRA
16	734	89.6	155	2 AAY28408	Aay28408 Human int
17	734	89.6	155	3 AAY92257	Aay92257 Human IL-
18	734	89.6	155	3 AAY45062	Aay45062 Human TAN
19	734	89.6	155	3 AAY96936	Aay96936 Human IL-
20	734	89.6	155	4 AAE06655	Aae06655 Human int
21	734	89.6	155	4 AAB66664	Aab66664 Protein e
22	734	89.6	155	4 AAB87601	Aab87601 Human PRO
23	734	89.6	155	4 AAB35262	Aab35262 Interleuk
24	734	89.6	155	4 AAB35260	Aab35260 Human IL-

25	734	89.6	155	5 ABG95926	Abg95926 Human sec
26	734	89.6	155	5 ABB84974	Abb84974 Human PRO
27	734	89.6	155	5 ABB95580	Abb95580 Human ang
28	734	89.6	155	5 ABP52018	Abp52018 NOVINTRA
29	734	89.6	155	5 ABP52034	Abp52034 NOVINTRA
30	734	89.6	155	5 ABP52047	Abp52047 NOVINTRA
31	734	89.6	155	6 ABB90951	Abb90951 Novel hum
32	734	89.6	155	6 ABO34010	Abu34010 Human sec
33	734	89.6	155	6 ABU72027	Abu72027 Novel hum
34	734	89.6	155	6 ABP97770	Abp97770 Amro aci
35	734	89.6	155	6 ABU71581	Abu71581 Human sec
36	734	89.6	155	6 ABU72362	Abu72362 Human PRO
37	734	89.6	155	6 ABU91035	Abu91035 Human PRO
38	734	89.6	155	6 ABO27356	Abu27356 Human sec
39	734	89.6	155	6 ABU92551	Abu92551 Human sec
40	734	89.6	155	6 ABU81221	Abu81221 Human sec
41	734	89.6	155	6 ABO53335	Abu53335 Novel hum
42	734	89.6	155	6 ABU98338	Abu98338 Novel hum
43	734	89.6	155	6 ABU89343	Abu89343 Novel hum
44	734	89.6	155	6 ABU82550	Abu82550 Novel hum
45	734	89.6	155	6 ABU96514	Abu96514 Human PRO

ALIGNMENTS

RESULT 1
AAW86284
ID AAW86284 standard; protein; 156 AA.
XX
AC
XX
AC AAW86284;
DT 19-FEB-1999 (first entry)
XX
DE Rodent interleukin (IL)-1 delta polypeptide.
XX
KW Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
KW inflammatory response; immune system; diagnosis; agonist; antagonist;
KW chemokine.
XX
OS Mus sp.
XX
PN W09847921-A1.
XX
PD 29-OCT-1998.
XX
PF 17-APR-1998; 98WO-US006879.
XX
PR 21-APR-1997; 97US-00837627.
PR 06-AUG-1997; 97US-0055111P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hedrick JA, Sana TR, Bazan JF, Kastelein RA;
XX WPI, 1998-609976/51.
DR N-PSDB; AAV71958.
XX
PT Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g. regulating
XX the immune system and inflammatory responses.
XX
PS Claim 1; Page 89-90; 113pp; English.
XX
CC This represents a rodent interleukin (IL)-1 delta polypeptide. The
CC invention relates to a recombinant polypeptide that specifically binds
CC polyclonal antibodies (Abs) generated against a 12 consecutive amino acid
CC segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these
CC IL polypeptides are used to regulate a cell involved in an inflammatory
CC response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are
CC used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and
CC the corresponding nucleic acids regulate development and/or the immune
CC system, and can be used to diagnose and treat conditions associated with
CC abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1

CC epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
 CC IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
 CC epsilon polypeptides may be used as a soluble polypeptide or as a fusion
 CC protein with another cytokine or chemokine

XX Sequence 156 AA;

Query Match 100.0%; Score 819; DB 2; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAALKVLYLHNNQTLAAGLHAERVIKGEISVVPNRALDASISPVIL 60
 DB 1 MMVLSGALCFRMDKSAALKVLYLHNNQTLAAGLHAERVIKGEISVVPNRALDASISPVIL 60
 QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAESKSFPTFYRDMGLTSSPESAAVPGM 120
 DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAESKSFPTFYRDMGLTSSPESAAVPGM 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 2

AAV28407
 ID AAV28407 standard; protein; 156 AA.

XX AAV28407;

XX 28-SEP-1999 (first entry)

XX Mouse interleukin 1 delta.

XX Interleukin 1 delta; IL-1 delta; glaucoma; ectodermal dysplasia;

XX insulin-dependent diabetes mellitus; wrinkly skin syndrome;

XX T-cell leukemia; lymphoma; tibial muscular dystrophy.

XX Mus musculus.

XX WO935268-A1.

XX 15-JUL-1999.

XX 08-JAN-1999; 99WO-US000514.

XX 09-JAN-1998; 98US-0071074P.

XX 01-JUN-1998; 98US-0087393P.

XX (IMMV) IMMUNEX CORP.

XX Sims JE;

XX WPI, 1999-458310/38.

XX N-PSDB; AAX89431.

XX Murine and Human interleukin 1 delta DNA, polypeptides and its fragments,
 XX useful as molecular weight markers.

XX Claim 1; Page 67; 72pp; English.

XX The present sequence represents mouse interleukin 1 delta (IL-1 delta).

XX IL-1 delta proteins are useful for the determination of the molecular
 XX weight of a sample protein. The protein and its fragments are useful as
 XX controls for peptide fragmentation. This is useful for determining the
 XX isoelectric point of a sample protein. Antibodies generated against IL-1
 XX delta and its fragmented peptides can be used to enhance the accuracy of
 XX these molecular weight markers to determine the apparent molecular weight
 XX of a sample protein. IL-1 delta can be used to

XX screen for potential inhibitors of activity associated with IL-1 delta
 XX and isoelectric point of a sample protein. IL-1 delta can also be used as therapeutic
 XX counter-structure molecules. IL-1 delta can also be used as therapeutic
 XX agents for the treatment of diseases mediated by IL-1 delta. IL-1 delta
 XX may be used as a reagent in studying the interleukin 1 (IL-1) signalling

CC pathway, or as a reagent to block IL-1 signalling. The IL-1 delta coding
 CC sequences can be used to identify human chromosome 2, and to identify
 CC genes associated with certain diseases, especially with region 2q11-12,
 CC including glaucoma, ectodermal dysplasia, insulin-dependent diabetes
 CC mellitus, wrinkly skin syndrome, T-cell leukemia/ lymphoma and tibial
 CC muscular dystrophy

XX Sequence 156 AA;

Query Match 100.0%; Score 819; DB 2; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAALKVLYLHNNQTLAAGLHAERVIKGEISVVPNRALDASISPVIL 60
 DB 1 MMVLSGALCFRMDKSAALKVLYLHNNQTLAAGLHAERVIKGEISVVPNRALDASISPVIL 60
 QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAESKSFPTFYRDMGLTSSPESAAVPGM 120
 DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAESKSFPTFYRDMGLTSSPESAAVPGM 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 3

AAV92260
 ID AAV92260 standard; protein; 156 AA.

XX AAV92260;

XX 10-AUG-2000 (first entry)

XX Murine IL-1 homologue, zll1a3.

XX Generic; interleukin-1; IL-1; homologue; zll1a3; anti-inflammatory;

XX antagonist; pro-inflammatory; agonist; immunomodulator; antiarthritic;

XX antirheumatic; osteopetrotic; antipsoriatic; antibacterial; cytostatic;

XX immunosuppressive; antitumor; antidiabetic; nephrotropic; vasotropic;

XX vulnary; 2q14.

XX Mus musculus.

XX WO200020595-A1.

XX 13-APR-2000.

XX 08-OCT-1999; 99WO-US023533.

XX 08-OCT-1998; 98US-00169745.

XX (ZYMO) ZYMOGENETICS INC.

XX Shepard PO, West RR, Clegg CH;

XX WPI; 2000-303780/26.

XX N-PSDB; AAA09198.

XX Proteins useful for treatment of inflammatory conditions such as
 XX rheumatoid arthritis and psoriasis are agonists or antagonists forms of
 XX new interleukin-1 homologue.

XX Example 7; Page 59-60; 64pp; English.

XX This shows an interleukin-1 (IL-1) homologue, designated zll1a3. A 350 bp
 XX probe generated from the DNA sequence by PCR using AAA09199-200 was used
 XX to analyze human northern blots. It is believed that zll1a3 acts through
 XX IL-1 receptors. In general, zll1a3 proteins having a Lys residue at
 XX position 148 will have anti-inflammatory activity (e.g. AAV92256), whilst
 XX those having Asp (see AAV92254) or Glu at this position will have pro-
 XX inflammatory action. Zll1a3 is used to modulate an immune response in an
 XX animal (claimed). Antagonists zll1a3 forms may be used to treat or

CC prevent chronic inflammatory diseases such as rheumatoid arthritis,
CC osteoarthritis and Lyme arthritis, psoriasis, to reduce tissue damage
CC after ischemia, to treat septic shock, graft-versus-host disease and
CC leukemia. The antagonists may also alleviate inflammatory bowel disease
CC including Crohn's disease and ulcerative colitis, insulin-dependent
CC diabetes mellitus, acute pancreatitis, glomerulonephritis and cerebral
CC ischemia. Agonist forms of zllia may promote wound healing by IL-1
CC effects on growth factor secretion and cell proliferation. They may also
CC treat infections, especially gastrointestinal infections
CC
SQ Sequence 156 AA;
Query Match 100.0%; Score 819; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVLSGALCFRMDKSAKLYLHNNQLAGLHAKEYIKGEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAKLYLHNNQLAGLHAKEYIKGEISVVPNRALDASLSPVIL 60
QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYAKESKSFPPYRDDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYAKESKSFPPYRDDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFYQCCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFYQCCD 156
RESULT 4
AAV5061
ID AAV5061 standard; protein; 156 AA.
AC AAV45061;
XX
DT 31-MAY-2000 (first entry)
XX
DE Murine TANGO-93 protein.
XX
KW TANGO-93; cytokine; mouse; secreted protein; IL-1 expression; cancer;
KW Interleukin-1 receptor antagonist; IL-1ra; inflammation; antiaesthetic;
KW immunosuppressive; antirheumatic; antipsoriatic; asthma;
KW antiinflammatory; antibacterial; antiulcer; cytostatic; immunomodulator;
KW osteopathic; dermatological; antidiabetic; psoriasis; ulcerative colitis;
KW graft vs-host disease; rheumatoid arthritis; inflammatory bowel disease;
KW septic shock; cachexia; Crohn's disease; chronic myelogenous leukemia;
KW liver disease; diabetes; osteoarthritis; Hodgkin's disease; Lyme disease;
KW autoimmune disease; myasthenia gravis; pharmacogenomic; diagnosis;
KW systemic lupus erythematosus; forensic; transgenic animal.
XX
OS Mus sp.
XX
PN MO200008045-A2.
XX
PD 17-FEB-2000.
XX
PF 06-AUG-1999; 99WO-US017886.
XX
PR 07-AUG-1998; 98US-00131263.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Pan Y;
XX
DR WPI; 2000-205669/18.
XX
DR N-PSDB; AAZ50811.
XX
PT Isolated nucleic acid sequences encoding TANGO-93 polypeptide useful for
XX treating a variety of cellular processes e.g. asthma, rheumatoid
XX arthritis, psoriasis and autoimmune diseases.
XX
PS Claim 9; Fig 1; 113pp; English.
XX

CC The present sequence is the murine TANGO-93, a secreted protein, that
CC belongs to the cytokine superfamily. It plays a role similar to secreted
CC Interleukin-1 receptor antagonist (IL-1ra) and its expression is
CC developmentally regulated in liver, heart and bone marrow. TANGO-93
CC modulates immune mediated inflammation and IL-1 gene or protein
CC expression. TANGO-93 is useful as a modulating agent for regulating
CC cellular processes like asthma, graft vs-host disease, rheumatoid
CC arthritis, psoriasis, inflammatory bowel disease, septic shock,
CC ulcerative colitis, Crohn's disease, chronic myelogenous leukemia,
CC cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme disease,
CC cachexia, and autoimmune diseases e.g. myasthenia gravis, autoimmune
CC diabetes and systemic lupus erythematosus. Partial TANGO-93 sequences are
CC useful in forensic biology, for diagnostic and prognostic assays
CC prophylactic and therapeutic treatment and pharmacogenomics. The DNA
CC sequences are useful as hybridisation probes and primers, for isolation
CC of TANGO-93 sequence and for the creation of transgenic animals
CC
SQ Sequence 156 AA;
Query Match 100.0%; Score 819; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMVLSGALCFRMDKSAKLYLHNNQLAGLHAKEYIKGEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAKLYLHNNQLAGLHAKEYIKGEISVVPNRALDASLSPVIL 60
QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYAKESKSFPPYRDDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYAKESKSFPPYRDDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFYQCCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFYQCCD 156
RESULT 5
ABU62869
ID ABU62869 standard; protein; 156 AA.
AC ABU62869;
XX
DT 11-SRP-2003 (first entry)
XX
DE Mouse secreted protein TANGO-93.
XX
KW Mouse; TANGO-93; secreted protein; antiaesthetic; immunosuppressive;
KW antirheumatic; antiarthritic; antiinflammatory; antipsoriatic;
KW cytostatic; hepatotropic; antidiabetic; dermatological; gene therapy;
KW cytokine superfamily; asthma; graft versus-host disease; cancer;
KW rheumatoid arthritis; psoriasis; inflammatory bowel disease;
KW septic shock; ulcerative colitis; Crohn's disease; liver disease;
KW chronic myelogenous leukemia; Hodgkin's disease; Lyme's disease;
KW cachexia; autoimmune diabetes; systemic lupus erythematosus.
XX
OS Mus musculus.
XX
PN US2003059892-A1.
XX
PD 27-MAR-2003.
XX
PF 09-OCT-2002; 2002US-00267791.
XX
PR 07-AUG-1998; 98US-00131263.
XX
PR 06-AUG-1999; 99US-00369693.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Pan Y;
XX
DR WPI; 2003-521914/49.
XX
DR N-PSDB; ACD26633, ACD26634.
XX

PT New TANGO-93 nucleic acid molecules and polypeptides useful for treating
 PT asthma, graft versus-host disease, rheumatoid arthritis, psoriasis,
 PT inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's
 PT disease, cancer.

XX Claim 8; Fig 1; 43pp; English.

XX The invention describes an isolated nucleic acid molecule (I) designated
 CC as TANGO-93, a secreted protein predicted to be a member of the cytokine
 CC superfamily. The polynucleotides, polypeptides compounds and methods are
 CC useful for treating asthma, graft versus-host disease, septic shock,
 CC arthritis, psoriasis, inflammatory bowel disease, ulcerative colitis,
 CC ulcerative colitis, Crohn's disease, chronic myelogenous leukaemia,
 CC cancer, liver disease, Hodgkin's disease, Lyme's disease, cachexia,
 CC autoimmune diabetes or systemic lupus erythematosus. This is the amino
 CC acid sequence of mouse TANGO-93

XX Sequence 156 AA;

Query Match 100.0%; Score 819; DB 7; Length 156;

Best Local Similarity 100.0%; Pred. No. 1, 1e-86; Mismatches 0; Indels 0; Gaps 0;

Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGLHAKEYIKGEISVVPNRALDASISPVIL 60
 DB 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGLHAKEYIKGEISVVPNRALDASISPVIL 60
 QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAAYPGW 120
 DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAAYPGW 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDPTFYFOCCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDPTFYFOCCD 156

RESULT 6

ID ADJ88315 standard; protein; 156 AA.

AC ADJ88315;

DT 06-MAY-2004 (first entry)

XX Mouse interleukin-1delta protein.

XX Interleukin-1zeta; gene therapy; immune system; haematopoietic cell;

KW inflammatory disorder; infection; allergy; cancer; mouse.

XX Mus musculus.

XX US680380-B1.

XX 20-JAN-2004.

XX 17-SBP-1999; 99US-00398412.

XX 18-SBP-1998; 98US-0100948P.

XX (SCHB) SCHERING CORP.

XX Tilmans JC;

XX WPI; 2004-189656/18.

XX New nucleic acid molecules encoding mammalian interleukin-1 polypeptides,
 PT useful for diagnosing, preventing or treating diseases associated with
 PT abnormal expression of interleukin, e.g. inflammation, infection or
 PT cancer.

XX Disclosure; SEQ ID NO 13, 36pp; English.

XX The invention relates to an isolated or recombinant nucleic acid encoding

CC interleukin-1zeta polypeptide. The invention is useful in gene therapy.

CC The composition and methods are useful in diagnosing or treating
 CC degenerative or abnormal conditions which directly or indirectly involve
 CC development, differentiation or function, e.g. of the immune system
 CC and/or haematopoietic cells. The invention may also be used for
 CC preventing or treating other diseases or disorders associated with
 CC abnormal expression or triggering of response to the interleukin, such as
 CC inflammatory disorders, infection, allergies or cancer. The present
 CC sequence is mouse interleukin-1delta.

XX Sequence 156 AA;

Query Match 100.0%; Score 819; DB 8; Length 156;

Best Local Similarity 100.0%; Pred. No. 1, 1e-86; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGLHAKEYIKGEISVVPNRALDASISPVIL 60
 DB 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGLHAKEYIKGEISVVPNRALDASISPVIL 60
 QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAAYPGW 120
 DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAAYPGW 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDPTFYFOCCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDPTFYFOCCD 156

RESULT 7

ID AD004688 standard; protein; 156 AA.

AC AD004688;

DT 29-JUL-2004 (first entry)

XX Mouse interleukin-1d.

XX Interleukin-1d; IL-1d; immune system; inflammatory reaction;

KW immunological disorder; mouse.

XX Mus sp.

XX Location/Qualifiers

FT Misc-difference 16 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 32 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 48 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 64 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 80 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 96 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 112 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 128 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

FT Misc-difference 144 /note= "Represented by incomplete 3-letter code in

FT sequence listing"

PN US2004087766-A1.
 XX
 PD 06-MAY-2004.
 XX
 XX
 PF 27-OCT-2003; 2003US-00694978.
 XX
 PR 18-SEP-1998; 98US-0100948P.
 PR 17-SEP-1999; 99US-00398412.
 XX
 PA (TIMA/) TIMANS J C.
 XX
 XX Timans JC;
 PI
 DR WPI; 2004-374758/35.
 XX
 PT New isolated or recombinant interleukin-1 zeta polypeptide and related
 PT reagents such as antibodies, useful for treating inflammatory disease and
 PT as probes for diagnosing immunological disorders.
 XX
 PS Disclosure; SEQ ID NO 13; 42pp; English.
 XX
 CC The invention relates to interleukin-1 zeta polypeptide and
 CC polynucleotide. The agonist or antagonist of the interleukin-1 zeta is
 CC useful in modulating a cell that is involved in inflammatory response.
 CC The peptide fragments of IL-1 zeta are useful in research and diagnostic
 CC tools in the study of inflammatory reactions to antigenic challenge and
 CC the development of more effective anti-inflammatory therapeutics.
 CC Interleukin-1 zeta is useful in regulation and/or development of immune
 CC system. A polynucleotide encoding IL-1 zeta is useful for detecting the
 CC expression level of the polypeptide in a patient suspected of having an
 CC immunological disorder. The present sequence is mouse interleukin-1d.
 CC Note: The present sequence is shown in Sequence Listing and pages 6-7 of
 CC the specification. However, the sequence given in sequence listing has
 CC incomplete 3-letter codes for several amino acids.
 XX
 SQ Sequence 156 AA;
 Query Match 100.0%; Score 819; DB 8; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVLSGALCFRMDLSALKVLYLHNNQLAGLHAERKVIKGEISVVPNRALDASLSVIL 60
 DB 1 MMVLSGALCFRMDLSALKVLYLHNNQLAGLHAERKVIKGEISVVPNRALDASLSVIL 60
 QY 61 GVQGSQCCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSPESAAYPGW 120
 DB 61 GVQGSQCCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSPESAAYPGW 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
 RESULT 8
 ID ADQ98213 standard; protein; 156 AA.
 XX
 AC ADQ98213;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Mouse TANGO-93.
 XX
 KW mouse; TANGO-93; asthma; graft-versus-host disease; rheumatoid arthritis;
 KW psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis;
 KW Crohn's disease; chronic myelogenous leukemia; cancer; liver disease;
 KW Hodgkin's disease; osteoarthritis; Lyme disease; cachexia;
 KW autoimmune disease; myasthenia gravis; autoimmune diabetes;
 KW systemic lupus erythematosus.
 XX
 OS Mus sp.
 XX

PN US2004142420-A1.
 XX
 PD 22-JUL-2004.
 XX
 XX
 PF 12-DEC-2003; 2003US-00734985.
 XX
 PR 07-AUG-1998; 98US-00131263.
 PR 06-AUG-1999; 99US-00369693.
 PR 29-APR-2002; 2002US-00134410.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Pan Y;
 PI
 DR WPI; 2004-579909/56.
 DR N-PSDB; ADQ98212.
 XX
 PT New isolated TANGO-93 nucleic acids and proteins, useful for diagnosing,
 PT screening, or treating asthma, rheumatoid arthritis, psoriasis,
 PT inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's
 PT disease, cancer, or liver disease.
 XX
 PS Claim 8; SEQ ID NO 2; 39pp; English.
 XX
 CC The invention relates to an isolated TANGO-93 nucleic acid. The nucleic
 CC acids and polypeptides are useful for diagnosing, screening, or treating
 CC disorders having an aberrant TANGO-93 activity or expression. Diseases
 CC include asthma, graft-versus-host disease, rheumatoid arthritis,
 CC psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis,
 CC Crohn's disease, chronic myelogenous leukemia, cancer, liver disease,
 CC Hodgkin's disease, osteoarthritis, Lyme disease, cachexia, or autoimmune
 CC disease, e.g. myasthenia gravis, autoimmune diabetes, or systemic lupus
 CC erythematosus. The present sequence represents the amino acid sequence of
 CC mouse TANGO-93.
 XX
 SQ Sequence 156 AA;
 Query Match 100.0%; Score 819; DB 8; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVLSGALCFRMDLSALKVLYLHNNQLAGLHAERKVIKGEISVVPNRALDASLSVIL 60
 DB 1 MMVLSGALCFRMDLSALKVLYLHNNQLAGLHAERKVIKGEISVVPNRALDASLSVIL 60
 QY 61 GVQGSQCCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSPESAAYPGW 120
 DB 61 GVQGSQCCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSPESAAYPGW 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
 RESULT 9
 ID AAY96937 standard; protein; 155 AA.
 XX
 AC AAY96937;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Murine IL-1 receptor antagonist 3.
 XX
 KW IL-1Ra3; interleukin-1 receptor antagonist-3; IL-11p; osteopathic;
 KW interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
 KW anti-arthritic; antimicrobial; respiratory; anti-schismic; vaccine;
 KW dermatological; immunomodulatory; gastrointestinal; gene therapy.
 XX
 OS Mus sp.
 XX
 PN WO2000039297-A2.
 XX

PD 06-JUL-2000.
 XX
 PF 22-DEC-1999; 99WO-US030720.
 XX
 PR 23-DEC-1998; 98US-0113430P.
 PR 22-JAN-1999; 99US-0116843P.
 PR 13-APR-1999; 99US-0129122P.
 XX
 PA (GENENTECH INC.
 PI Goddard A, Pan J;
 PI WPI; 2000-452395/39.
 DR N-PSDB; AAA51599.
 XX
 PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
 PT preventing and treating e.g. inflammation, asthma and psoriasis.
 PS Claim 22; Fig 9A-B, 143pp; English.
 XX
 XX An isolated nucleic acid molecule encoding an interleukin-1-like
 CC polypeptide (IL-11p) that retains one or more activities of the peptide
 CC from which it is derived, such as the IL-18R binding activity of a human
 CC interleukin-1 receptor antagonist-1 (IL-1Ra) polypeptide, is new. The
 CC nucleic acid may be used in molecular engineering applications, e.g.
 CC hybridization assays and chromosome and gene mapping studies, for
 CC recombinantly producing the IL-11p polypeptide or for producing gene
 CC knock out animals to study the role of the protein in metabolism and
 CC disease processes (conversely, gene therapy protocols may be used to
 CC supplement a patient's production of the polypeptide or to rectify
 CC mutations that lead to the production of an active peptide). The
 CC peptides produced may be used to screen for and produce modulators (e.g.
 CC antibodies) of IL-11p protein expression and activity which may be used to
 CC treat disorders associated with inappropriate IL-11p expression and
 CC activity, such as inflammatory disorders, asthma, arthritis,
 CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
 CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
 CC psoriasis, graft versus host disease and/or inflammatory bowel disease
 XX
 SQ Sequence 155 AA;
 Query Match 99.4%; Score 814; DB 3; Length 155;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MVLGALCFPMKDSALKVLYLHNNQLAGLHAERVIKGEISVPPRALDASLSPVILG 61
 DB 1 MVLGALCFPMKDSALKVLYLHNNQLAGLHAERVIKGEISVPPRALDASLSPVILG 60
 QY 62 VGGSGCSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 121
 DB 61 VGGSGCSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 120
 QY 122 LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 156
 DB 121 LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 155
 RESULT 10
 AAB6672
 ID AAB6672 standard; protein; 155 AA.
 XX
 AC AAB6672;
 XX
 DT 05-APR-2001 (first entry)
 XX
 DE Invention related sequence #4.
 XX
 KM Interleukin; IL-1 receptor; cancer; inflammation.
 XX
 OS Mus sp.
 XX
 PN WO200102571-A2.

XX
 PD 11-JAN-2001.
 XX
 PF 07-JUL-2000; 2000WO-US018710.
 XX
 PR 07-JUL-1999; 99US-00348942.
 PR 13-OCT-1999; 99US-00417455.
 PR 08-DEC-1999; 99US-00457626.
 PR 10-MAR-2000; 2000US-00523552.
 PR 22-MAY-2000; 2000US-00576008.
 XX
 PA (HYSEQ INC.
 PI Ford J, Pace A;
 PI WPI; 2001-071582/08.
 DR
 XX
 PT Isolated nucleic acids encoding interleukin-1 (IL-1) receptor antagonist
 PT proteins (referred as IL-1H1), useful in the treatment of cancer, e.g.
 PT breast adenocarcinoma and brain tumors, and an inflammatory disease
 PT mediated by IL-18.
 PS Disclosure; Page 177; 179pp; English.
 XX
 CC The present invention relates to interleukin (IL)-1 receptor antagonist
 CC proteins. IL-1H1 is useful for treating cancer, an inflammatory disease
 CC mediated by IL-18, inflammation resulting from infection or allergic
 CC reactions, and inflammation associated with chronic bronchitis,
 CC arthritis, diabetes or endothermia
 XX
 SQ Sequence 155 AA;
 Query Match 99.4%; Score 814; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MVLGALCFPMKDSALKVLYLHNNQLAGLHAERVIKGEISVPPRALDASLSPVILG 61
 DB 1 MVLGALCFPMKDSALKVLYLHNNQLAGLHAERVIKGEISVPPRALDASLSPVILG 60
 QY 62 VGGSGCSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 121
 DB 61 VGGSGCSCGTEKGPILKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 120
 QY 122 LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 156
 DB 121 LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 155
 RESULT 11
 AAB48828
 ID AAB48828 standard; protein; 155 AA.
 XX
 AC AAB48828;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Murine interleukin-1 homologue 3 (IL-1H3).
 XX
 KM Interleukin-1 homologue 3; IL-1H3; mouse; murine; drug screening;
 KM agonist; antagonist; human disease; chronic inflammation;
 KM acute inflammation; septicemia; autoimmune disease; psoriasis;
 KM inflammatory bowel disease; arthritis; transplant rejection; infection;
 KM graft versus host disease; acute respiratory distress syndrome; allergy;
 KM asthma; restenosis; stroke; ischemia; brain injury; AIDS; bone disease;
 KM osteoporosis; cancer; lymphoproliferative disorder; atherosclerosis;
 KM congestive heart failure; Alzheimer's disease; immunosuppressive;
 KM antimicrobial; neuroprotective.
 XX
 OS Mus musculus.
 XX
 PN WO200071583-A1.

PD 30-NOV-2000.
 XX
 PF 24-MAY-2000; 2000MO-US014200.
 XX
 PR 24-MAY-1999; 99US-0135599P.
 PR 23-MAY-2000; 2000US-00577715.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Smith RF, Young PR, McDonnell PC, Halsey W;
 XX WPI; 2001-025138/03.
 DR N-PSDB; AAC81700.
 XX
 PT Murine interleukin-1 homolog polypeptide used for screening modulators of
 PT the polypeptide which can be used for treating autoimmune diseases,
 XX cancer, brain injury and bone disorders.
 PS Claim 2; Page 28-29; 31pp; English.
 XX
 CC The invention relates to murine interleukin-1 homologue 3 (IL-1H3;
 CC AAB48828) and nucleic acids which encode it (cDNA given in AAC81700).
 CC including nucleic acid sequences with at least 95% identity to AAC81700.
 CC The invention also relates to expression vectors and host cells
 CC comprising murine IL-1H3 nucleic acids, the recombinant production of
 CC murine IL-1H3, methods of screening for modulators of IL-1H3 activity,
 CC and IL-1H3 agonists and antagonists thus identified. IL-1H3 agonists and
 CC antagonists are of use for treating human diseases such as chronic or
 CC acute inflammation, septicemia, autoimmune diseases (e.g., inflammatory
 CC bowel disease, psoriasis and arthritis), transplant rejection, graft
 CC versus host disease, infection, stroke, ischemia, acute respiratory
 CC distress syndrome, allergies, asthma, restenosis, brain injury, AIDS,
 CC bone diseases (e.g., osteoporosis), cancers (e.g., lymphoproliferative
 CC disorders), congestive heart failure, atherosclerosis and Alzheimer's
 CC disease. The present sequence represents murine IL-1H3
 CC
 SQ Sequence 155 AA;
 Query Match 99.4%; Score 814; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MVLGALCFRMKDSALKVLYLHNNQLAGLHAERKVIKGEISVVPNRALDASLSPVILG 61
 DB 1 MVLGALCFRMKDSALKVLYLHNNQLAGLHAERKVIKGEISVVPNRALDASLSPVILG 60
 QY 62 VGGSGQCSGCGTEKGPILKLEPVNIMELYLGAESKSTFYRRDMGLTSSPSSAAYPGWF 121
 DB 61 VGGSGQCSGCGTEKGPILKLEPVNIMELYLGAESKSTFYRRDMGLTSSPSSAAYPGWF 120
 QY 122 LCTSPDADQPVRLTQIPEDPAMDAPITDPTFYQQCD 156
 DB 121 LCTSPDADQPVRLTQIPEDPAMDAPITDPTFYQQCD 155
 RESULT 12
 AAB35261
 ID AAB35261 standard; protein; 155 AA.
 XX
 AC AAB35261;
 XX
 DT 08-MAY-2001 (first entry)
 XX
 DE Murine IL-1L1.
 XX
 KM Mouse; IL-1L1, interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;
 KM chromosome 2q13; inflammatory disease; heart disease; Graves' disease;
 KM rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
 KM osteoporosis; systemic lupus erythematosus.
 XX
 OS Mus sp.
 XX

PN W0200105974-A2.
 XX
 PD 25-JAN-2001.
 XX
 PF 17-JUL-2000; 2000MO-US019508.
 XX
 PR 16-JUL-1999; 99US-0144298P.
 XX
 PA (INTE-) INTERLEUKIN GENETICS INC.
 PA Nicklin M, Barton J;
 PI WPI; 2001-091974/10.
 DR
 XX
 PT Nucleic acids encoding human and murine interleukin-1L1 polypeptides
 PT useful for controlling inflammatory processes.
 XX
 PS Claim 11; Fig 3; 150pp; English.
 XX
 CC The present invention provides the protein and coding sequences of the
 CC human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is
 CC located between the IL-1beta and IL-1receptor genes at human chromosome
 CC 2q13. The sequences are useful in the diagnosis, prevention and treatment
 CC of heart disease, cancer and inflammatory diseases such as rheumatoid
 CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,
 CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,
 CC severe periodontal disease and pregnancy complications. The present
 CC sequence is the murine IL-1L1 protein
 CC
 SQ Sequence 155 AA;
 Query Match 99.4%; Score 814; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 4e-86;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MVLGALCFRMKDSALKVLYLHNNQLAGLHAERKVIKGEISVVPNRALDASLSPVILG 61
 DB 1 MVLGALCFRMKDSALKVLYLHNNQLAGLHAERKVIKGEISVVPNRALDASLSPVILG 60
 QY 62 VGGSGQCSGCGTEKGPILKLEPVNIMELYLGAESKSTFYRRDMGLTSSPSSAAYPGWF 121
 DB 61 VGGSGQCSGCGTEKGPILKLEPVNIMELYLGAESKSTFYRRDMGLTSSPSSAAYPGWF 120
 QY 122 LCTSPDADQPVRLTQIPEDPAMDAPITDPTFYQQCD 156
 DB 121 LCTSPDADQPVRLTQIPEDPAMDAPITDPTFYQQCD 155
 RESULT 13
 AAE06663
 ID AAE06663 standard; protein; 154 AA.
 XX
 AC AAE06663;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Mouse interleukin-1delta (IL-1delta) protein.
 XX
 KM Mouse; interleukin-1delta; IL-1delta; virucide; hepatotropic; fever;
 KM immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
 KM autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
 KM psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
 XX
 OS Mus sp.
 XX
 PN W0200157219-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 01-FEB-2001; 2001MO-US003285.
 XX
 PR 02-FEB-2000; 2000US-0179638P.
 XX

PA (SCHE) SCHERING CORP.

PI Debets JEMA, Timans JC, Bazan JF, Kaetelein RA;

XX WPI; 2001-488886/53.

XX Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT polypeptide useful for treating conditions exhibiting abnormal expression
PT of interleukin such as immunological disorders, tumor and allergy.

XX Disclosure; Fig 1; 103pp; English.

XX The invention relates to recombinant antigenic interleukin-1 like
CC molecules and their corresponding nucleic acid sequences, designated as
CC interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon). IL
CC -1delta and IL-1epsilon are useful for treating conditions exhibiting
CC abnormal expression of the interleukin such as immunological disorders,
CC tumour, inflammatory diseases and infectious diseases (e.g., pulmonary
CC allergy, autoimmune diseases and hepatitis, and viral infections such as
CC tuberculosis, leprosy, fulminant hepatitis, and AIDS).
CC HIV). The invention also relates to methods of using the composition
CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC utilities. IL-1delta is used as an immunogen for the production of
CC antisera or antibodies and an IL-1delta, for the interleukin or its
CC fragment. The purified interleukin is used as a reagent to detect any
CC antibodies generated in response to the presence of elevated levels of
CC expression, or immunological disorders which lead to antibody production
CC to the endogenous cytokine. The invention also contemplates the use of
CC competitive drug screening assays. The present sequence is mouse
CC interleukin-1delta (IL-1delta) protein related to the invention

SQ Sequence 154 AA;

Query Match 98.8%; Score 809; DB 4; Length 154;

Best Local Similarity 100.0%; Pred. No. 1.5e-85;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSGALCFRMKDSALKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVILGV 62
DB 1 VLSGALCFRMKDSALKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVILGV 60
QY 63 QGSGGSCSCGTEKGPILKLEPVNIMELYLGAKESKSFYRRDGLTSSFSAAYPGW 122
DB 61 QGSGGSCSCGTEKGPILKLEPVNIMELYLGAKESKSFYRRDGLTSSFSAAYPGW 120
QY 123 CTSPADQPVRLTQIPEDPAMDAPITDYPFOCD 156
DB 121 CTSPADQPVRLTQIPEDPAMDAPITDYPFOCD 154

RESULT 14

ADL15877 standard; protein; 156 AA.

ADL15877;

01-JUL-2004 (first entry)

Human interleukin-1z (IL-1z).

KM antiinflammatory; interleukin 1 zeta; IL-1 zeta; immunogen;
KM antisera production; antibody production; anti-inflammatory; human;
KM interleukin 1z; IL-1z.

OS Homo sapiens.

US2004068099-A1.

08-APR-2004.

27-OCT-2003; 2003US-00695195.

PR 18-SEP-1998; 98US-0100948P.

PR 17-SEP-1999; 99US-00398412.

PA (TIMA) TIMANS J C.

XX Timans JC;

XX WPI; 2004-304623/28.

XX Novel isolated or recombinant interleukin 1 zeta polypeptide useful as
PT immunogen for producing specific antibodies or for developing anti-
PT inflammatory therapeutics.

XX Disclosure; SEQ ID NO 13; 42pp; English.

XX The invention describes an isolated or recombinant interleukin 1 zeta
CC polypeptide (I) that specifically binds to polyclonal antibodies
CC generated against at least a 12 consecutive amino acid segment of two
CC fully defined sequences (S1) and (S2) having 218 amino acids as given in
CC the specification and comprises at least one sequence chosen from (S1)
CC and (S2). Also described are: a fusion protein comprising (I) or its
CC sequence; a detection of another cytokine or chemokine; a binding compound
CC (II) an antigen binding site from an antibody, which specifically binds
CC to (I); a composition of matter comprising a sterile polypeptide (I) or
CC (II); (I) or (II) and a carrier such as an aqueous compound e.g., water,
CC saline and/or buffer, where the carrier is formulated for oral, rectal,
CC nasal, topical or parental administration; an isolated or recombinant
CC nucleic acid (III) that encodes (I) or several antigenic peptides of (S1)
CC or (S2); a cell (IV) transformed with (III); a method of modulating a
CC cell involved in an inflammatory response, by contacting the cell with an
CC agonist or antagonist of (I); a kit comprising a compartment of (I), (II)
CC or (III) and/or instructions for use or disposal of reagents in the kit;
CC and producing an antibody as immunogen for producing antisera or specific
CC complex. (I) is useful for developing more effective anti-inflammatory
CC antibodies or useful for developing more effective anti-inflammatory
CC therapeutics. This is the amino acid sequence of a human interleukin 1z
CC polypeptide to which the novel interleukin of the invention is related.

SQ Sequence 156 AA;

Query Match 98.5%; Score 807; DB 8; Length 156;

Best Local Similarity 98.1%; Pred. No. 2.6e-85;

Matches 153; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMTLSGALCFRMKDSALKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60
DB 1 MMTLSGALCFRMKDSALKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60
QY 61 GVOXGSCSCGTEKGPILKLEPVNIMELYLGAKESKSFYRRDGLTSSFSAAYPGW 120
DB 61 GVOXGSCSCGTEKGPILKLEPVNIMELYLGAKESKSFYRRDGLTSSFSAAYPGW 120
QY 121 FLCTSPADQPVRLTQIPEDPAMDAPITDYPFOCD 156
DB 121 FLCTSPADQPVRLTQIPEDPAMDAPITDYPFOCD 156

RESULT 15

ABP52012 standard; protein; 146 AA.

ABP52012;

10-OCT-2002 (first entry)

NOVINTRA A homologous amino acid sequence SEQ ID NO:55.

KM Human; transmembrane protein; neuromedin protein; gonadotropin protein;
KM interleukin-1 receptor antagonist; interleukin-1 epsilon; NOVX;
KM IL-1 epsilon; IL-1 receptor antagonist; lung disease; noctropic;
KM cytosolic; neuroprotective; antiinflammatory; antibacterial;
KM immunosuppressive; cerebroprotective; antidiabetic; antiarthritic;

KM antiasthmatic; antiallergic; gene therapy; antibody-based therapy;
 KM cell signalling disorder; haematopoietic disorder; endocrine; muscle;
 KM neurodegenerative disorder; neurological disorder; cancer; melanoma;
 KM central nervous system cancer; reproductive development disorder; asthma;
 KM metabolic function disorder; bone metabolism; structure disorder; stroke;
 KM inflammatory response disorder; immune regulation disorder; septic shock;
 KM diabetes; arthritis; lung cancer; emphysema; allergic lung irritation;
 KM lung inflammation.

OS Homo sapiens.

PN US002068279-A1.

XX 06-JUN-2002.

XX 05-DEC-2000; 2000US-00730617.

XX 06-DEC-1999; 99US-0169056P.

XX 09-DEC-1999; 99US-0169866P.

XX 10-DEC-1999; 99US-0169866P.

XX 12-JAN-2000; 2000US-0175740P.

PA (CURA-) CURAGEN CORP.

PI Burgess C, Prayaga SK, Shimkels RA, Raetelli L, Zerhusen B;

PI Mezes P;

XX WPI; 2002-582472/62.

PT New NOVX proteins for diagnosing or treating cell signaling, immune
 PT response, hematopoietic, neurodegenerative, muscle, endocrine, bone, and
 PT reproductive development disorders.

PS Disclosure; Fig 10B; 110pp; English.

XX The present invention describes an isolated NOVX polypeptide, chosen from
 CC human transmembrane (NOVTRAN), neuromedin (NOVNEUR), gonadotropin
 CC (NOVGON), interleukin-1 (IL-1) receptor antagonist (NOVINTRA A and B),
 CC and IL-1 epsilon proteins. NOVX polypeptides have nootropic, cyostatic,
 CC neuroprotective, antiinflammatory, antibacterial, immunosuppressive,
 CC cerebroprotective, antidiabetic, antirheumatic, antiasthmatic and
 CC antiallergic activities, and can be used in gene therapy and antibody-
 CC based therapy. NOVX polypeptides, nucleic acid (I) encoding them and an
 CC antibody (III) that binds the polypeptide, are useful for treating or
 CC preventing a NOVX protein-associated disorder in humans. NOVTRAN can be
 CC used in the treatment of a cell signalling disorder, such as, a
 CC haematopoietic disorder or a neurodegenerative disorder. NOVNEUR can be
 CC used in the treatment of an endocrine, muscle, neurological disorder,
 CC central nervous system cancer, breast, colon, ovarian, kidney, prostate
 CC or thyroid cancer. NOVGON can be used in the treatment of a reproductive
 CC development disorder, metabolic function disorder or melanoma. NOVINTRA
 CC proteins can be used in the treatment of and a bone metabolism or
 CC structure disorder, an inflammatory response disorder, an immune
 CC regulation disorder, septic shock, stroke, diabetes, arthritis or cancer.
 CC An agent which modulates the expression or activity of a human IL-1
 CC epsilon protein is useful for treating a lung disease such as lung
 CC cancer, asthma, emphysema, allergic lung irritation and lung inflammation
 CC in a mammal. ABQ73996 to ABQ74027 and ABP51981 to ABP52048 represent
 CC sequences used in the exemplification of the present invention

XX SQ Sequence 146 AA;

Query Match 93.8%; Score 768; DB 5; Length 146;

Best Local Similarity 100.0%; Pred. No. 8.4e-81;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CFRMDSALKVLVYHNNQILAGLHAKEYIKGEISVVPNRALDASLSPVILGVGGSGQC 68
 Db 1 CFRMDSALKVLVYHNNQILAGLHAKEYIKGEISVVPNRALDASLSPVILGVGGSGQC 60
 QY 69 LSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGWFLCTSPRA 128

Db 61 LSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGWFLCTSPRA 120
 QY 129 DQVRLTQIPEDPAMDAPITDPYFQQ 154
 Db 121 DQVRLTQIPEDPAMDAPITDPYFQQ 146

Search completed: April 5, 2006, 15:08:44
 Job time : 192 secs

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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:05:57 ; Search time 23 Seconds
(without alignments)
652.601 Million cell updates/sec

Title: US-09-770-528-2
Perfect score: 819
Sequence: 1 MVLISGALCFRMDKDSALKVLT.....IPEDPAMDAPITDPTFYQQCD 156

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	734	89.6	155	2 JC7104	interleukin-1 rece
2	319.5	39.0	178	2 A44610	interleukin-1 rece
3	307.5	37.5	177	2 A30368	interleukin-1 rece
4	297.5	37.5	180	2 A39386	interleukin-1 rece
5	297.5	36.3	178	2 C40956	interleukin-1 rece
6	289.5	35.3	177	2 A54377	interleukin-1 rece
7	137.5	16.8	266	1 S23010	interleukin-1 beta
8	134.5	16.4	266	1 ICBO1B	interleukin-1 beta
9	129	15.8	267	1 JN0724	interleukin-1 beta
10	128.5	15.7	214	2 JC5646	interleukin-1 beta
11	128	15.6	269	1 I55969	interleukin-1 beta
12	127	15.5	267	2 S38373	interleukin-1 beta
13	122	14.9	269	1 ICHUIB	interleukin-1 beta
14	119	14.5	268	1 A30584	interleukin-1 beta
15	84	10.3	259	2 P95843	conserved hypotet
16	84	10.3	1427	2 I51669	tumor suppressor -
17	84	10.3	1447	2 A54100	tumor suppressor p
18	80	9.8	364	2 T05401	hypothetical prote
19	80	9.8	437	2 A41357	ATP sulfurylase -
20	78	9.5	344	2 A41357	PC gamma (Igg) rec
21	78	9.5	374	2 A39878	PC gamma (Igg) rec
22	76.5	9.3	551	2 C86506	methionyl-tRNA syn
23	76.5	9.3	551	2 H81552	methionyl-tRNA syn
24	75.5	9.2	264	2 A75354	hypothetical prote
25	75.5	9.2	1034	2 S36758	mg11 protein - mou
26	75.5	9.2	1116	2 T42213	m-tomomya, isoform
27	74	9.0	982	2 T19526	hypothetical prote
28	73.5	9.0	551	2 H72117	methionine-tRNA 11
29	73	8.9	310	2 T33457	hypothetical prote

30	73	8.9	632	2 T45471	dnak-type molecule
31	72.5	8.9	815	2 T36671	probable helicase
32	72.5	8.9	1272	2 S26180	neurofascin - chic
33	72	8.8	911	2 T01353	serine/threonine p
34	71.5	8.7	204	2 G97071	folate-dependent p
35	71.5	8.7	282	2 AF0902	dihydropteroreate sy
36	71.5	8.7	488	2 A87374	hypothetical prote
37	71.5	8.7	621	2 D96554	hypothetical prote
38	71	8.7	268	1 A61246	interleukin-1 alph
39	71	8.7	268	1 ICBO1A	interleukin-1 alph
40	71	8.7	333	2 AH2179	dnak protein (limpo
41	71	8.7	640	2 S37394	dnak-type molecule
42	70.5	8.6	550	2 G70597	probable proteinas
43	70.5	8.6	608	2 T05741	dnak-type molecule
44	70.5	8.6	663	2 T03581	dnak-type molecule
45	70.5	8.6	663	2 T04080	dnak-type molecule

ALIGNMENTS

RESULT 1

JC7104
interleukin-1 receptor antagonist - human
C/Species: Homo sapiens (man)
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: JC7104
R/Milero, J.U.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Forc
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A/Title: IL1RH1: A novel interleukin-1 receptor antagonist gene.
A/Reference number: JC7104; M0ID:99443727; PMID:10512743
A/Molecule type: mRNA
A/Accession: JC7104
A/Residues: 1-155 <MUL>
A/Cross-references: UNIPROT:Q9UBH0; UNIPARC:UPI0000034E98; GB:AF186094; NID:G6049804;
C/Genetics:
A/Gene: il1rh1
A/Map position: 2q14
C/Keywords: macrophage

Query Match 89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2.3e-67;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 MVLISGALCFRMDKDSALKVLT.....IPEDPAMDAPITDPTFYQQCD 61
DB 1 MVLISGALCFRMDKDSALKVLT.....IPEDPAMDAPITDPTFYQQCD 60
QY 62 VQGSQCLSCGVQEBPTLTLEPVNIMELYAKESKSFYRRDGLTSSFSBSAAYPGWF 121
DB 61 VQGSQCLSCGVQEBPTLTLEPVNIMELYAKESKSFYRRDGLTSSFSBSAAYPGWF 120
QY 122 ICTSPRADQPVRLTQIPEDPAMDAPITDPTFYQQCD 156
DB 121 ICTSPRADQPVRLTQIPEDPAMDAPITDPTFYQQCD 155

RESULT 2

A44610
interleukin-1 receptor antagonist precursor - mouse
N/Alternate names: IL-1Ra
C/Species: Mus musculus (house mouse)
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C/Accession: A44610; B40956; A49031; I56106; I52970
R/Matsushima, H.; Rousset, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A/Title: Cloning and expression of murine interleukin-1 receptor antagonist in macroph
A/Reference number: A44610; M0ID:91316273; PMID:1830498
A/Accession: A44610
A/Molecule type: mRNA
A/Residues: 1-178 <MUL>
A/Cross-references: UNIPROT:P25085; UNIPARC:UPI00000041CB; GB:M64404; NID:G198296; PI
R/Bisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomps

Proc.Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991

A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family.

A:Reference number: A40956; MUID:91271363; PMID:1828896

A:Accession: B40956

A:Molecule type: DNA

A:Residues: 7-178 <EIS>

A:Cross-references: UNIPARC:UPI000016CE4B; GB:M63100; NID:9198389; PIDN:AAA39310.1; PID:R.Shuck, M.E.; Bessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.

Bur J. Immunol. 21, 275-2780, 1991

A:Title: Cloning, heterologous expression and characterization of murine interleukin 1

A:Reference number: A49031; MUID:92037824; PMID:1834470

A:Accession: A49031

A:Molecule type: mRNA

A:Residues: 23-178 <SHU>

A:Cross-references: UNIPARC:UPI0000170C6C; GB:S64082; NID:9238584; PIDN:AAB20265.1; PID:A.Experimental source: peritoneal macrophages, JCR strain

A>Note: Sequence extracted from NCBI Backbone (NCBI:64082, NCBI:P:64085)

Rizahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.

J. Immunol. 146, 4228-4233, 1991

A:Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene mapping

A:Reference number: 156106; MUID:91250712; PMID:1828262

A:Accession: 156106

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-178 <RES>

A:Cross-references: UNIPARC:UPI00000041CB; GB:M74294; NID:9196387; PIDN:AAA39309.1; PID:R.Zahedi, K.A.; Uhlir, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.

Cytokine 6, 1-9, 1994

A:Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulation

A:Reference number: 152970; MUID:94271931; PMID:8003626

A:Accession: 152970

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-178 <RE2>

A:Cross-references: UNIPARC:UPI00000041CB; GB:L32838; NID:9487864; PIDN:AAA20576.1; PID:C.Genetics:

A:Gene: IL-1rn

A:Introns: 40/2; 70/1; 107/3

C:Superfamily: interleukin-1

C:Keywords: cytokine receptor

F.1-26/Domain: signal sequence #status predicted <SIG>

F.27-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>

Query Match 39.0%; Score 319.5; DB 2; Length 178;

Best Local Similarity 48.6%; Pred. No. 4.4e-25;

Matches 71; Conservative 17; Mismatches 49; Indels 9; Gaps 3;

QY 10 FMKQSAKLVLYAHNNOLLAGGLHAEKVIGKEISVVPRAADALSLPVLGVGGSQCL 69

DB 39 FRIWITNQKTFPIRRNQILAGYLQGNITLAEKIDMV-----IDLHVFGLIHGKCKL 93

QY 70 SCGTETKGP1-LKLEPVNIMELYLGAESKSFPTFYRRDGLTSSFSFAAYPGMFLCTSPDA 128

DB 94 SCAGSGDDIKIQLEEVNITDLISKNKEEDRFTFIRSEKPTTSSFAACPGWFLCTTLEA 153

QY 129 DQPVRLTQIPEDPDAMDAPITDFYFOQ 154

DB 154 DRPVSLTNTPEEP--LIVTKFYFOE 176

RESULT 3

A30368

Interleukin-1 receptor antagonist secreted form precursor - human

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1990 #sequence, revision 07-Jun-1990 #text_change 09-Jul-2004

C:Accession: A40956; J17894; A30368; S08160; S08159; A37822

R. Eisenberg, S.P.; Brewer, M.T.; Venderber, E.; Heimdahl, P.; Brandhuber, B.J.; Thompson, Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991

A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family

A:Reference number: A40956; MUID:91271363; PMID:1828896

A:Accession: A40956

A:Molecule type: DNA

A:Residues: 1-177 <EIS>

A:Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist
A:Reference number: 137894; MUID:92338323; PMID:1385887
A:Accession: 137894
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-177 <LEN>
A:Cross-references: UNIPARC:UPI000003475A; EMBL:X64532; NID:G33798; PIDN:CAA5832.1; I
R:Cartier, D.B.; Deibel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; LaBorde, A.L.; Slightom,
U.G.; Siew, L.C.; Hardee, M.M.; Zutterer-Neely, H.A.; Reardon, I.M.; Héritierson, R.L.;
Nature 344, 633-638, 1990
A:Title: Purification, cloning, expression and biological characterization of an inter
A:Reference number: A30368; MUID:90220867; PMID:2139180
A:Accession: A30368
A:Molecule type: mRNA
A:Residues: 1-177 <CNR>
A:Cross-references: UNIPARC:UPI000003475A; GB:X53296; NID:932578; PIDN:CAA37386.1; PI
A:Note: parts of this sequence, including the amino end of the mature protein, were CC
R:Elemeberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.;
Nature 343, 341-346, 1990
A:Title: Primary structure and functional expression from complementary DNA of a human
A:Reference number: S08160; MUID:90136921; PMID:2137201
A:Accession: S08160
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-177 <E12>
A:Cross-references: UNIPARC:UPI000003475A; GB:X52015; NID:932576; PIDN:CAA36262.1; PI
R:Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joellin, F.G.; Dripps, D.J.; Heimdahl, P.L.;
Nature 343, 336-340, 1990
A:Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor
A:Reference number: S08159; MUID:90136920; PMID:2137200
A:Accession: S08159
A:Molecule type: protein
A:Residues: 26-75; 97-108; 110-116; 120-131; 163-176 <HAN>
A:Cross-references: UNIPARC:UPI00001588B6; UNIPARC:UPI000017672F; UNIPARC:UPI000017672F;
R:Rienkowsk, M.J.; Beesall, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Labori
J. Biol. Chem. 265, 14503-14511, 1990
A:Title: Purification and characterization of interleukin 1 receptor level antagonist
A:Reference number: A37822; MUID:90354444; PMID:2143761
A:Accession: A37822
A:Molecule type: protein
A:Residues: 26-52; 70-77; 122-127; 170-175 <B1E>
A:Cross-references: UNIPARC:UPI000017673; UNIPARC:UPI00001767; UNIPARC:UPI00001767;
A:Experimental source: culture medium, PMA-stimulated THP-1 cells
C:Comment: For an alternative splice form, see PIR:A39386
C:Genetics:
A:Gene: GDB:IL1RN
A:Cross-references: GDB:125897; OMIM:147679
A:Map position: 2d14.2-2d14.2
A:Introns: 39/2; 69/1; 106/3
C:Superfamily: interleukin-1
C:Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprote
F.1-5/Domain: signal sequence #status predicted <SIG>
F.26-177/Product: interleukin-1 receptor antagonist #status experimental <MAT>
F.109/Binding site: carbohydrate (Aam) (covalent) #status experimental

Query Match	37.5%;	Score 307.5;	DB 2;	Length 177;
Best Local Similarity	48.0%;	Pred. No. 7.3e-24;		
Matches	72;	Conservative 16;	Mismatches 45;	Indels 17; Gaps 5;
10	PMKRSALAVLYLHNHQLLAGGLHAKEVYKGEISVVPNRDLASLP--VILGVQGSQ	67		
38	PRIMVNOQTFFLRNNQVLAVGLQGNVNLKIDIVP-----IPHLFLGIGSKM	90		
68	CLISG---GTEKCPILKLEPVNIMELYLAKESKSPFFYRDMGLTSPFSAAYGWFCT	124		
91	CLISCVKSGDET--LQLEAVNITDLSENRKQDRFAFIRSDSGPTISFSAACGWFICT	148		
125	SPKADQVRLTOIPEDPAMDAPITDFYFQO	154		
149	AKKADQPVSLTNMPE---GWATKTFQGE	175		

A/Accession: S23010
 A/Molecule type: mRNA
 A/Residues: 1-266 <S20>
 A/Cross-references: UNIPROT:P21621; UNIPARC:UPI0000030876; EMBL:X56972; NID:g1808; PIDN:R1Sargan, D.R. 1992
 A/Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an additional
 submitted to the EMBL Data Library, May 1992
 A/Accession: S43047
 A/Reference number: S43047
 A/Accession: S43047
 A/Molecule type: mRNA
 A/Residues: 1-13, 'C', '15-54', 'K', '56-63', 'A', '65-144', 'L', '146-266 <SAR>
 A/Cross-references: UNIPARC:UPI000016C4C5; EMBL:X54796; NID:g1273; PIDN:CAA38566.1; PID:R1Sargan, D.R. 1992
 A/Note: Nucleotide sequence of ovine interleukin-1 beta.
 A/Title: Nucleotide sequence of ovine interleukin-1 beta.
 A/Reference number: S13092; MUID:9108326; PMID:2263490
 A/Accession: S13092
 A/Molecule type: mRNA
 A/Residues: 1-13, 'C', '15-54', 'K', '56-61', 'S', '63', 'A', '65-144', 'L', '146-266 <FIS>
 A/Cross-references: UNIPARC:UPI0000173676; EMBL:X54796
 A/Note: the authors translated the codon AGT for residue 62 as Arg
 R1Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
 Immunology 74, 453-460, 1991
 A/Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
 A/Reference number: A61246; MUID:92120716; PMID:1769692
 A/Accession: B61246
 A/Molecule type: mRNA
 A/Residues: 1-144, 'L', '146-266 <AND>
 A/Cross-references: UNIPARC:UPI000002CD35
 A/Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
 ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
 C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1
 C/Genetics:
 A/Gene: IL-1-beta
 C/Superfamily: Interleukin-1
 C/Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
 C/KeyWord: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
 F:114-266/Product: interleukin-1 beta #status predicted <MAT>
 Query Match 16.8%; Score 137.5; DB 1; Length 266;
 Best Local Similarity 30.9%; Pred. No. 2.5e-06; Indels 17; Gaps 5;
 Matches 42; Conservative 24; Mismatches 53;
 QY 17 LKVLVYHNNQLLAGLHAEKVIKGEISVVPNRALDASLSPVILGVGGSCGCTGK 76
 DB 139 LKALHLPSQEMSRREVCMSFVQGEERD-----NKIPVALGIDKMLYLSC-VKKG 188
 QY 77 --PIKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFCTSPEDQPVRL 134
 DB 189 DTPILQLEEVDP-KPYVPRNMEKRFVYKTEIKNTVEFESVLYPNWYISTQIERPVFL 247
 QY 135 TQIPEDPAMDAPITDF 150
 DB 248 GRF----RGGDITDF 259
 RESULT 8
 ICBOLB
 Interleukin-1 beta precursor - bovine
 N/Alternate names: hematopoietin-1; IL-1 beta
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
 C/Accession: J10010; S01380
 R1Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.
 Mol. Immunol. 25, 429-437, 1988
 A/Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin
 A/Reference number: A94695; MUID:88318652; PMID:3261832
 A/Accession: J10010
 A/Molecule type: mRNA
 A/Residues: 1-266 <MAL>
 A/Cross-references: UNIPROT:P09428; UNIPARC:UPI0000167C08; GB:M37211; NID:g163200; PIDN:R1Leonig, S.R.; Plaggs, G.M.; Lawman, M.; Gray, P.W.
 Nucleic Acids Res. 16, 9054, 1988
 A/Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.

A/Reference number: S01380; MUID:89016591; PMID:3262866
 A/Accession: S01380
 A/Molecule type: mRNA
 A/Residues: 1-251, 'A', '253-266 <LEO>
 A/Cross-references: UNIPARC:UPI000003086F; EMBL:X12498; NID:g448; PIDN:CAA31018.1; PID:R1Leonig, S.R.; Plaggs, G.M.; Lawman, M.; Gray, P.W.
 A/Note: This protein is a cytokine that mediates a variety of immunoregulatory and
 C/Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
 ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
 C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1
 C/Superfamily: Interleukin-1
 C/Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
 F:114-266/Product: interleukin-1 beta #status predicted <MAT>
 Query Match 16.4%; Score 134.5; DB 1; Length 266;
 Best Local Similarity 30.9%; Pred. No. 5.1e-06;
 Matches 42; Conservative 23; Mismatches 54; Indels 17; Gaps 5;
 QY 17 LKVLVYHNNQLLAGLHAEKVIKGEISVVPNRALDASLSPVILGVGGSCGCTGK 76
 DB 139 LKALHLPSQEMSRREVCMSFVQGEERD-----NKIPVALGIDKMLYLSC-VKKG 188
 QY 77 --PIKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFCTSPEDQPVRL 134
 DB 189 DTPILQLEEVDP-KPYVPRNMEKRFVYKTEIKNTVEFESVLYPNWYISTQIERPVFL 247
 QY 135 TQIPEDPAMDAPITDF 150
 DB 248 GRF----RGGDITDF 259
 RESULT 9
 UN0724
 Interleukin-1 beta precursor - pig
 N/Alternate names: hematopoietin-1; IL-1 beta
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
 C/Accession: JN0724
 R1Huecher, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Mollitor, T.W.
 Gene 129, 285-289, 1993
 A/Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1
 A/Reference number: JN0724; MUID:93314975; PMID:8325511
 A/Accession: JN0724
 A/Molecule type: mRNA
 A/Residues: 1-267 <HUE>
 A/Cross-references: UNIPROT:P26889; UNIPARC:UPI0000030879; GB:M86725; NID:g164607; PI:R1Huecher, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Mollitor, T.W.
 A/Experimental source: alveolar macrophage
 A/Comment: This protein is a pleiotropic cytokine that mediates a variety of processes
 C/Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
 ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
 C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1
 C/Superfamily: Interleukin-1
 C/Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
 F:115-267/Product: interleukin-1 beta #status predicted <IL1>
 F:77/Binding site: myristate (lys) (covalent) #status predicted
 Query Match 15.8%; Score 129; DB 1; Length 267;
 Best Local Similarity 29.9%; Pred. No. 1.9e-05;
 Matches 47; Conservative 26; Mismatches 48; Indels 36; Gaps 8;
 QY 2 MVLGALCFPMKDSALKVLYHNNQLLAGLHAEKVIKGEISVVPNRALDASLS 56
 DB 132 LVYLA-----PHMLKALH-----LITGLDKREVCMSFVQGDSDN-----NKI 170
 QY 57 PVILGVGGSCGCTGKTPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESA 115
 DB 171 PVTLGIGKMLYSCVMKMDTPITQLSDID-PKPYPRNMEKRFVYKTEIKNTVEFESA 229
 QY 116 AYPGWFCTSPEDQPVRL--TQIPEDPAMDAPITDF 150
 DB 230 LYPNWYISTQIERPVFLGNSKGRD-----ITDF 260
 RESULT 10

JC5646
interleukin-1 beta - horse
C/Species: Equus caballus (domestic horse)
C/Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
A/Accession: JC5646
R/Kato, H.; Yonai, H.Y.; Ohnishi, T.; Watari, T.; Gotsuka, R.; Tsujimoto, H.; Hasegawa, A.
Gene 177, 11-16, 1996
A/Title: Identification of an alternatively spliced transcript of equine interleukin-1 beta
A/Reference number: JC5646; MUID:97080493; PMID:8921838
A/Accession: JC5646
A/Molecule type: mRNA
A/Residues: 1-214 <KAT>
A/Cross-references: UNIPROT:Q28386; UNIPARC:UPI000002ABD0; DDBJ:D42165; NID:g2463549; P
C/Comment: This protein mediates a variety of physiological response to infections and i
synthesis by hepatocytes, and stimulation of chondrocytes and synovial cells to produce
C/Superfamily: interleukin-1

Query Match 15.7%; Score 128.5; DB 2; Length 214;
Best Local Similarity 33.6%; Pred. No. 1.6e-05;
Matches 40; Conservative 16; Mismatches 44; Indels 19; Gaps 5;

Qy 38 IKGEISVVPNRALDASLPVLIQGGSGCCTGK-PILKLEPVNIMELYAKES 96
Db 108 VQGE-----ETDKIPALGIKKNLVISCGMKGKPTLQLETVD-ENTYKAKME 157
Qy 97 KSFTFRRDMLTSSFSAAVPGWFLCTSPADQPVRL--TQIPEDPAMDAPITDFYFQ 153
Db 158 KRFVFNKMEIKGNVEFSAMYPNMYISTQAEKSPVFLGNTRGRD-----ITDFIME 210

RESULT 11

I53969
interleukin-1 beta precursor - mouse
N/Alternate names: hematopoietin-1; IL-1 beta
C/Species: Mus musculus (house mouse)
C/Date: 26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
A/Accession: I53969; A24719; S13029
R/Gray, P.W.; Glaser, D.; Chen, E.; Goeddel, D.V.; Pennica, D.
J. Immunol. 137, 3644-3648, 1986
A/Title: Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for mu
A/Reference number: I53969; MUID:87058957; PMID:3491144
A/Accession: I53969
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-269 <RBS>
A/Cross-references: UNIPROT:P10749; UNIPARC:UPI00000190B; GB:M15131; NID:g198293; PIDN:
R/Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla, E.; Melli, M.
Nucleic Acids Res. 14, 9955-9963, 1986
A/Title: The murine interleukin-1 beta gene: structure and evolution.
A/Reference number: A24719; MUID:87117546; PMID:3492706
A/Accession: A24719
A/Molecule type: mRNA
A/Residues: 1-269 <TEL>
A/Cross-references: UNIPARC:UPI00000190B; GB:X04964; NID:g52666; PIDN:CA28637.1; PID:
R/Dunay, G.O.; Wilder, C.L.; Merenda, J.M.; Mccoll, A.S.; Geoghegan, K.F.; O'Leary, T.
FEBS Lett. 278, 98-102, 1991
A/Title: Reduction of biological activity of murine recombinant interleukin-1beta by sel
A/Reference number: S13029; MUID:91130610; PMID:1993481
A/Accession: S13029
A/Status: preliminary
A/Molecule type: protein
A/Residues: 118-269 <DAV>
A/Cross-references: UNIPARC:UPI0000054163
C/Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin-1alpha, is inactive.
C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C/Genetics:
A/Gene: IL-1-beta
C/Superfamily: interleukin-1
C/Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F/118-269/Product: interleukin-1 beta #status experimental <ILL>

Query Match 15.6%; Score 128; DB 1; Length 269;

Best Local Similarity 31.7%; Pred. No. 2.4e-05;
Matches 44; Conservative 23; Mismatches 50; Indels 22; Gaps 6;

Qy 8 LCPMKDSALKVLVYHNNOVLGGLHAEKVKGEISVVPNRALDASL----- 56
Db 123 LHYLRBQKSLVLSPEYELK-ALH-----LNGNT-----NQYIFSMSPVQGEBSNDKI 173
Qy 57 PVILVQGGSGCCTGK-PILKLEPVNIMELYAKESKFTFRRDMLTSSFSESA 115
Db 174 PVALGLKKNLVISCGMKDGPPTLQLESVPKQ-YPKKMKRFRVFNKIEVKSKEVES 232
Qy 116 AYPWFLCTSPADQPVRL 134
Db 233 EFPNMYISTQAEKHPVRL 251

RESULT 12

S38373
interleukin-1 beta precursor - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
A/Accession: S38373
R/Vanderbroeck, K.; Fiten, P.; Baeken, E.; Martens, E.; Janssen, A.; van Damme, J.; (Eur. J. Biochem. 217, 45-52, 1993
A/Title: Gene sequence, cDNA construction, expression in Escherichia coli and genetic
A/Reference number: S38373; MUID:94039070; PMID:8223584
A/Accession: S38373
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-267 <VAN>
A/Cross-references: UNIPROT:Q29082; UNIPARC:UPI0000030873; EMBL:X74568; NID:g407899;
C/Genetics:
A/Intons: 16/2; 33/3; 99/1; 154/1; 197/3
C/Superfamily: interleukin-1

Query Match 15.5%; Score 127; DB 2; Length 267;
Best Local Similarity 32.9%; Pred. No. 3e-05;
Matches 50; Conservative 21; Mismatches 55; Indels 26; Gaps 8;

Qy 2 MVLSGALCFPMKDSALKVLVYHNNOVLGGLHAEKVKGEISVVPNRALDASLPYL 61
Db 132 LVLAG-----PHEKALH-----LTKGLKREVPFC---MSFVQDDSDDKI-PTTLG 175
Qy 62 VQGGSGCCTGK-PILKLEPVNIMELYAKESKFTFRRDMLTSSFSAAVPGW 120
Db 176 IKGNLVISCGMKDGPPTLQLEVD-PKSYKDKMERGFYFVTKIKRVEFSALYPNW 234
Qy 121 FLCTSPADQPVRL--TQIPEDPAMDAPITDF 150
Db 235 YISTQAEKHPVFLGNSKGRD-----ITDF 260

RESULT 13

ICHT1B
interleukin-1 beta precursor [validated] - human
N/Alternate names: hematopoietin-1; IL-1 beta
C/Species: Homo sapiens (man)
C/Date: 28-Feb-1986 #sequence_revision 15-May-1998 #text_change 09-Jul-2004
A/Accession: A25542; A29019; A93601; A93601; I51852; I65300; I361332; B27616; A01648;
R/Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Atron, P.B.
Nucleic Acids Res. 14, 7897-7914, 1986
A/Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a
A/Reference number: A25542; MUID:87040762; PMID:3490654
A/Accession: A25542
A/Molecule type: DNA; mRNA
A/Residues: 1-5 'K'; 7-269 <CLA>
A/Cross-references: UNIPROT:P01584; UNIPARC:UPI0000030874; GB:X04500; NID:g33788
A/Note: the mRNA sequence had codon AAG for 6-bps, the DNA sequence had GAG for 6-GT
R/Bens, G.; Rauegi, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Melli, M.
Gene 52, 95-101, 1987
A/Title: Human interleukin-1 beta gene.
A/Reference number: A29019; MUID:87248099; PMID:2954882
A/Accession: A29019

A: Molecule type: DNA
A: Residues: 1-269 <BEN>
A: Cross-references: UNIPARC:UPI00000054161; GB:M15840; NID:q186281; PIDN:AAA4137.1; PID:Rauton, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Dinares Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A: Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A: Reference number: A94023; MUID:85088517; PMID:6083565
A: Accession: A94023
A: Molecule type: mRNA
A: Residues: 1-5, 'K', 7-269 <AUR>
A: Cross-references: UNIPARC:UPI00000030874; GB:K02770; NID:q186268; PIDN:AAA56106.1; PID:R. March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S. Nature 315, 641-647, 1985
A: Title: Cloning, sequence and expression of two distinct human interleukin-1 complement A: Reference number: A93561; MUID:85240547; PMID:2985698
A: Accession: A93561
A: Molecule type: mRNA
A: Residues: 1-269 <MAR>
A: Cross-references: UNIPARC:UPI00000054161; GB:X02533; NID:q33789; PIDN:CAA6372.1; PID:9 A: Note: parts of this sequence, including the amino end of the mature form, were confirm R. Webb, A.C.; Dinares, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; A: Adv. Gene Technol. 22, 339-340, 1985
A: Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A: Reference number: 151852
A: Accession: 151852
A: Molecule type: mRNA
A: Status: translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-5, 'K', 7-119, 'H', 21-110, 'O', 112-176, 'A', 178-213, 'P', 215-269 <WEB>
A: Cross-references: UNIPARC:UPI000016A0A; GB:M54933; NID:9186287; PIDN:AAA59136.1; PID: N. Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; Hara Biochem. Biophys. Res. Commun. 143, 345-352, 1987
A: Title: CDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
A: Reference number: 152217; MUID:87156769; PMID:3493774
A: Accession: 165200
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-269 <NIS>
A: Cross-references: UNIPARC:UPI00000054161; GB:M15330; NID:q186283; PIDN:AAA59135.1; PID: R. Kotenko, S.V.; Bulechko, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov, I.I.; S.A.; Vinetskii, Y.P.
Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989
A: Title: Cloning of the cDNA coding for human proliferin-leukin-1 alpha and prointerleukin A: Reference number: 138131; MUID:90249285; PMID:2635664
A: Accession: 138132
A: Status: translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-269 <KOT>
A: Status: translated from GB/EMBL/DBJ
A: Cross-references: UNIPARC:UPI00000054161; EMBL:X56087; NID:q35662; PIDN:CAA3567.1; PID: R. Zsebo, K.M.; Wpych, J.; Yusczenko, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, K. Blood 71, 962-968, 1988
A: Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic A: Reference number: A90732; MUID:88184226; PMID:3281727
A: Accession: B27616
A: Molecule type: Protein
A: Residues: 117-123, 'X', 125-126, 'X', 128 <ZSE>
A: Cross-references: UNIPARC:UPI0000017367D
R. Stevenson, F.T.; Burstein, S.L.; Fantom, C.; Locksley, R.M.; Lovett, D.H. Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
A: Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysines A: Reference number: A48293; MUID:93348250; PMID:8346241
A: Accession: A48293
A: Content: annotation; myristylation of lysines
R. Wanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S. Biochim. Biophys. Acta 1118, 25-35, 1991
A: Title: The role of arginine residues in interleukin 1 receptor binding.
A: Reference number: S19608; MUID:92110334; PMID:1837236
A: Content: annotation; type 1 IL-1 receptor interaction site
A: Note: modification of Arg-120 by phenylglyoxal blocks receptor binding
R. Clote, G.M.; Gronenborn, A.M.
A: Reference number: A50049; PDB:611B
submitted to the Brookhaven Protein Data Bank, January 1991
A: Content: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
R. Clote, G.M.; Wingfield, P.T.; Gronenborn, A.M.
Biochemistry 30, 2315-2323, 1991

A:Title: High-resolution three-dimensional structure of interleukin 1beta in solution
A:Reference number: A44675; MUID:91159409; PMID:2001363
A:Contents: annotation; (1)H-NMR structural determination
R:Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R.
J. Biol. Chem. 266, 7081-7086, 1991
A:Title: Structure-function mapping of interleukin 1 precursor. Cleavage leads to a
A:Reference number: A39774; MUID:91201363; PMID:2016316
A:Contents: annotation
R:Finzel, B.C.; Watenpugh, K.D.; Einspahr, H.M.
submitted to the Brookhaven Protein Data Bank, December 1989
A:Reference number: A50016; PMID:1111
A:Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269
R:Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpugh, K.D.; Einspahr, J. Mol. Biol. 209, 779-791, 1989
A:Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom resolution
A:Reference number: A44666; MUID:90064532; PMID:258509
A:Contents: annotation; X-ray crystallography, 2.0 angstroms
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleaved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin C:Genetics:
A:Gene: GDB:IL1B
A:Cross-references: GDB:120094; OMIM:147720
A:Map position: 2q13-2q21
A:Intons: 16/2; 33/3; 101/1; 156/1; 199/3
C:Superfamily: Interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macroph F:117-269/Product: interleukin-1 beta #status experimental <IL1>
F:76/Binding site: myristate (lys) (covalent) (partial) #status experimental
F:123/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match	14.9%;	Score 122;	DB 1;	Length 269;
Best Local Similarity	29.04;	Pred. No. 9,7e-05;		
Matches	45;	Conservative 25;	Mismatches 59;	Indels 26; Gaps 6;

Qy 2 MWLGGALCFPMKQDALKVYLYLHNNQLAGLHAEKVIKKEEISVVPNRALDASLSPVILG 61
Db 134 LVMNGPY-----ELKALHLQGDMEQGVMSVQGEESN-----DKIPVALG 177
Qy 62 VGGGSGQLSCG-TEKGPIKLLEFPVIMEDYLGAKESKSFYRRDNGLTSSPFAAYPCGW 120
Db 178 LKKNLNLSCVLDMDKPTQLGLSEVD-PKNVPRKGGMEKRFVFNKIEINNKLFESQAQPMW 236
Qy 121 FLCTSPADQPVRL--TQIPEDPAMAPITDPFQ 153
Db 237 YISTQAEINMPVFGLGTTKGQD-----ITDFTMQ 265

RESULT 14
A30584
interleukin-1 beta precursor - rabbit
N:Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 25-May-1989 #sequence revision 22-Nov-1996 #text_change 09-Jul-2004
R:Accession: A27714; A30584; J00082; A32166
R:Morris, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M. Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
A:Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potenti A:Reference number: A27714; MUID:88134238; PMID:2449207
A:Accession: A27714
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-268 <MOR>
A:Cross-references: UNIPROT:P14628; UNIPARC:UPI0000030877
R:Canon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Loebberger, C.; Dinarello J. Immunol. 142, 2299-2306, 1989
A:Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcrip A:Reference number: A30584; MUID:89176242; PMID:2784458
A:Accession: A30584
A:Molecule type: mRNA
A:Residues: 1-268 <CAN>
A:Cross-references: UNIPARC:UPI0000030877; GB:M26295; NID:G516632; PIDN:AAA1373.1; P R:Young, P.R.; Sylvestre, D.

Protein Eng. 2:545-551, 1989
A>Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and
A,Reference number: A84230; MUID:89315718; PMID:2787507
A,Accession: J00082
A,Molecule type: mRNA
A,Residues: 1-268 <YOUN>
A,Cross-references: UNIPARC:UPI0000030877
C,Comment: This protein lacks a conventional signal sequence for protein export. Cleaved form of interleukin-1-beta, unlike interleukin-1-alpha, is inactive.
C,Comment: Interleukin-1-beta precursor is less heavily myristoylated than interleukin-1-
C,Superfamily: interleukin-1
C,Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
P,117-268/Product: Interleukin-1 beta #status predicted <IUB>

Query Match	14.5%	Score 119	DB 1	Length 268
Best Local Similarity	30.6%	Pred. No. 0.00019		
Matches 41; Conservative	20; Mismatches 55;		Indels 18;	Gaps 4

QY 2 MVLGALCFRRKDSALKVLYHNNQLLAGGLHAEKVTKGEETSVVPRALDASLPVILG 61
: ||| : : : : : |||
Db 133 LVLSGT-----ELKALHNAENLQQVVFMSFVQGEESN-----DKIPVALG 176

Dy 62 VGGSGQCLSC-GTEKGPILKEPVMIMELYCAKESSESFTFPARRDMGLTSSPESSAAYPCW 120C
::: ||| : | : ||| : :: : ||| : |
Db 177 LRGNLYLSCVMDKPFTLGESVD-PNRRYPKKMKERFVFNNKIEIKDKLEFFESAQFPNW 235S

QY	121	FLCTSP	EQPVRL	134
	:	:	:	:
Db	236	YISTSQ	TEYMPVFL	249

RESULT 15

P95843
 conserved hypothesized protein SMB20011 [Imported] - *Sinorhizobium meliloti* (strain 1021)
 C:Species: *Sinorhizobium meliloti*
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: P95843
 R:Fthan, T.W.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vortholler, F.J.; Hernan-
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A>Title: The complete sequence of the 1,663-kb pSymb megaplasmid from the N2-fixing endo-
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: P95843
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-259 <KIR>
 A:Cross-references: UNIPROT:O92XE8; UNIPARC:UPI00000CB3A2; GB:AL591985; PIDN:CAC48414.1
 A:Experimental source: Strain 1021, megaplasmid pSymb
 R:Gallbert, F.; Fthan, T.W.; Long, S.R.; Hubler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 P.; Del, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaulc, P.; Vandenbol, M.; Vortholler, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.;
 A>Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: SMB20011
 A:Genome: plasmid

Query Match	10.3%	Score 84	DB 2	Length 259
Best Local Similarity	27.2%	Pred. No. 0.66		
Matches 41	Conservative 18	Mismatches 46	Indels 46	Gaps 7

DQ

14 DSALKVLYH-----NNOLLAGGHAEEKVIKGEETSVENRALDASLPYILGVGG 65
| | | | : | | | | : | : |
DB 97 DQKAEEVDRLRRRRPRGSNVAVLACGTSAEELIEGMITGV-----GATFPEPVALLIGL 150
| | | | : | | | | : | : |

```
QY      66 S Q C L A S C G T E N G P I L K L E P V N M E L Y C A K E S F T F R D M G I T S ---S F E S A A Y P P G A F   12
       : | : : | | | : : | | | : : | | |
Db     151 A I C I D N F S -----E G M S I G E L T D E E R K N A --K R R T L G W T S L I G I S L F V S A V A G N F   199
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QY 122 LCTSP EADQPVRLTQIPEDPAWDAPITDFYF 152

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Db      200  LKLG-----LAQ-----PVGFLP 21
Search completed: April  5, 2006, 15:06:28
Job time : 24 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:05:45 ; Search time 230 Seconds

(without alignments)
478,532 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 819

Sequence: 1 MMVLGALCRMDALKT.....IPEDPAWDAPITDFPQQCD 156

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80-*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	819	100.0	156	1	IL1F5_MOUSE
2	734	89.6	155	1	IL1F5_MOUSE
3	319.5	39.0	159	2	Q542M1_MOUSE
4	319.5	39.0	178	1	IL1RA_MOUSE
5	319.5	39.0	178	2	Q542C7_MOUSE
6	317.5	38.8	159	2	Q8CGM1_MOUSE
7	312	38.1	152	1	IL1RA_MOUSE
8	309	37.7	152	2	Q56AT8_MOUSE
9	307.5	37.5	177	1	IL1RA_MOUSE
10	307.5	37.5	180	2	Q53SC2_MOUSE
11	305.5	37.3	177	1	IL1RA_MOUSE
12	305.5	37.3	177	1	IL1RA_MOUSE
13	304	37.1	152	1	IL1RA_MOUSE
14	304	37.1	152	2	Q53SR9_MOUSE
15	301.5	36.8	174	1	IL1RA_MOUSE
16	299.5	36.6	177	1	IL1RA_MOUSE
17	297.5	36.3	177	1	IL1RA_MOUSE
18	289.5	35.3	177	1	IL1RA_MOUSE
19	285.5	34.9	176	1	IL1RA_MOUSE
20	269.5	32.9	177	1	IL1RA_MOUSE
21	213.5	26.1	82	2	Q6PUJ3_PIG
22	190.5	23.3	72	2	Q77771_HORSE
23	189.5	23.1	218	1	IL1F7_MOUSE
24	184.5	22.5	138	2	Q4R3X2_MOUSE
25	182.5	22.3	219	2	Q7RU00_MOUSE
26	181.5	22.2	160	1	IL1F6_MOUSE
27	169.5	20.7	267	1	Q73909_CHICK
28	167.5	20.5	158	1	IL1F6_MOUSE
29	167.5	20.5	158	1	Q5BLR4_MOUSE
30	167.5	20.5	158	2	Q53SR7_MOUSE
31	165.5	20.2	183	1	IL1F8_MOUSE

32	157	19.2	159	1	IL1F9_MOUSE	Q9NZH8_homo_sapien
33	157	19.2	159	2	Q56B91_MOUSE	Q56B91_homo_sapien
34	155	18.9	230	2	Q712X7_ORNAN	Q712X7_ornithorhyn
35	148.5	18.1	246	2	Q98SG5_SCOMX	Q98SG5_scomichalm
36	145	17.7	253	2	Q5K4R2_GADMO	Q5K4R2_gadus_morhu
37	143	17.5	283	2	Q711M3_XENIA	Q711M3_xenopus_lae
38	143	17.5	283	2	Q9PVZ5_XENIA	Q9PVZ5_xenopus_lae
39	143	17.5	283	2	Q569Q8_XENIA	Q569Q8_xenopus_lae
40	137.5	16.8	266	1	IL1B_SHEEP	Q21621_ovis_aries
41	137	16.7	268	1	IL1B_HORSE	Q21621_ovis_aries
42	136.5	16.7	266	1	IL1B_CEREL	Q21621_ovis_aries
43	135.5	16.5	266	2	Q5R458_BUBBU	Q5R458_bubalus_bub
44	134.5	16.4	266	2	IL1B_BOVIN	Q5R458_bubalus_bub
45	132	16.1	247	2	Q8QGW0_PAROL	Q8QGW0_parallelchth

ALIGNMENTS

RESULT 1
ID IL1F5_MOUSE STANDARD; PRT; 156 AA.
AC Q9QYX1; Q9UG2;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Interleukin-1 family member 5 (IL-1F5) (Interleukin-1 delta) (IL-1 delta) (Interleukin-1-like protein 1) (IL-1L1) (Interleukin-1 H1) (IL-1H1) (Interleukin-1 homolog 3) (IL-1H3).
GN Name=IL1F5; Synonyms=Fltd, Il1h3, Il1h1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
[2]
[3]
[4]
NUCLEOTIDE SEQUENCE.
RX MEDLINE=20545212; PubMed=11091146;
DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMUJ3299>3.0.CO;2-S;
RA Barton J.L., Herbst R., Bosisto D., Higgins L., Nicklin M.J.H.;
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities";
RL Eur. J. Immunol. 30:3299-3308(2000).
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 X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 3-156, AND DISULFIDE BOND.
 Pubmed:12974628; DOI=10.1021/bi0341197;
 Dunn E.F., Gay N.J., Bristow A.F., Gearing D.P., O'Neill L.A.J.,
 Pei X.Y.,
 "High-resolution structure of murine interleukin 1 homologue IL-1F5
 reveals unique loop conformations for receptor binding specificity,"
 Biochemistry 42:10938-10944(2003).
 CC -1- FUNCTION: Is a highly and a specific antagonist of the IL-1
 receptor-related protein 2-mediated response to interleukin 1
 family member 9 (IL1P9). Could constitute part of an independent
 signaling system analogous to interleukin-1 alpha (IL-1A), beta
 (IL-1B), receptor agonist and interleukin-1 receptor type I (IL-
 1RI), that is present in epithelial barriers and takes part in
 local inflammatory response (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly abundant in embryonic tissue and
 tissues containing epithelial cells.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

Best Local Similarity 100.0%; Pred. No. 7,6e-77;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMTLSGALCFRMDKSLKVLITRNNOILAGLHAERKIKGEISVVPNRALDASLSPVIL 60
 Db 1 MMTLSGALCFRMDKSLKVLITRNNOILAGLHAERKIKGEISVVPNRALDASLSPVIL 60
 QY 61 GVGQGGSCGLSCGKEKPIILKLEPVNIMELYLGAKESESFFPYRRDMGLTSSFESAAYPGW 120
 Db 61 GVGQGGSCGLSCGKEKPIILKLEPVNIMELYLGAKESESFFPYRRDMGLTSSFESAAYPGW 120
 QY 121 FLCTSPADQPVRLTOIPEDPADAPITDFYFOOCD 156
 Db 121 FLCTSPADQPVRLTOIPEDPADAPITDFYFOOCD 156
 RESULT 2
 IL1F5 HUMAN STANDARD; PRT; 155 AA.
 AC Q9UBH0; Q56AT9; Q7RTZ6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Interleukin 1 family member 5 (IL-1F5) (interleukin-1 delta) (IL-1
 delta) (PIL1 delta) (interleukin-1-like protein 1) (IL-1L1)
 DE (interleukin-1 H1) (IL-1H1) (interleukin-1 receptor antagonist
 homolog 1) (IL-1ra homolog 1) (IL-1 related protein 3) (IL-1RP3).
 GN Name=IL1F5; Synonyms=PIL1D, IL1H1, IL1L1, IL1RP3;
 GN ORFNames=UNQ1896/PRO4342;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 OX [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Placenta;
 RX MEDLINE=20092888; Pubmed=10625660; DOI=10.1074/jbc.275.2.1169;
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Kudin M., Garke K.E.,
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 RP TISSUE=Fetal skin;
 RX MEDLINE=99443727; Pubmed=10512743; DOI=10.1006/birc.1999.1440;
 RA Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
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 RX MEDLINE=20545212; Pubmed=11093146;
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 RP MEDLINE=20318623; Pubmed=10860666; DOI=10.1006/geno.2000.6184;
 RX Bustfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,

Query Match 100.0%; Score 819; DB 1; Length 156;

RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.,
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 RT "SeattleSNP: NHGRI H66682 program for genomic applications, UW-
 RT FRCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>)."
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 [9]
 RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15815621; DOI=10.1038/nature03466;
 RA Hillier L.W., Graves T.A., Fulton R.S., Fulton L.A., Pepin K.H.,
 RA Minx P., Wagner-McPherson C., Layman D., Wyllie K., Sekhon M.,
 RA Becker M.C., Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E.,
 RA Krentzki C., Oddy L., Du H., Sun H., Bradshaw-Cordum H., Ali J.,
 RA Carter J., Cordes M., Harris A., Isak A., van Brunt A., Nguyen C.,
 RA Du P., Courtney L., Kalicki J., Ozersky P., Abbott S., Armstrong J.,
 RA Belter E.A., Caruso L., Cedroni M., Cotton M., Davidson T., Desai A.,
 RA Elliott G., Erb T., Fronick C., Gaige T., Haakenson W., Haglund K.,
 RA Holmes A., Harkins R., Kim K., Kruchowski S.S., Strong C.M.,
 RA Gwella N., Goyea E., Hou S., Levy A., Martinka S., Mead K.,
 RA McElellan M.D., Meyer R., Randall-Maher J., Tomlinson C.,
 RA Dauphin-Kohlberg S., Kozlowski-Reilly A., Shan N.,
 RA Leonard S., Pearson C., Trani L., Radionenko M., Waligorski J.E.,
 RA Wang C., Rock S.M., Tin-Mollam A.-M., Maupin R., Latreille P.,
 RA Wendt M.C., Yang S.-P., Pohl C., Wallis J.W., Spieth J., Bieri T.A.,
 RA Berkowicz N., Nelson J.O., Osborne J., Ding L., Meyer R., Sabo A.,
 RA Shokland Y., Simha P., Woldmann P.E., Cook K.L., Hickenbotham M.T.,
 RA Elidori J., Williams D., Jones T.A., She X., Ciccarelli F.D.,
 RA Izaurrealde E., Taylor J., Schmutz J., Myers R.M., Cox D.R., Huang X.,
 RA McPherson J.D., Mardis E.R., Clifton S.W., Warren W.C.,
 RA Chinwalla A.T., Eddy S.R., Marra M.A., Ovcharenko I., Furey T.S.,
 RA Miller W., Richter E.E., Bork P., Suyama M., Torrents D.,
 RA Waterston R.H., Wilson R.K.;
 RT "Generation and annotation of the DNA sequences of human chromosomes 2
 RT and 4." ;
 RL Nature 434:724-731(2005).
 [10]
 RA NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX TISSUE=Placenta; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schneitz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohilyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Schermer A., Schein U.E., Jones S.D.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: is a highly and a specific antagonist of the IL-1
 CC receptor-related protein 2-mediated response to interleukin 1
 CC family member 9 (IL19). Could constitute part of an independent
 CC signaling system analogous to interleukin-1 alpha (IL-1A), beta
 CC (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-
 CC 1R1), that is present in epithelial barriers and takes part in
 CC local inflammatory response.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in keratinocytes but
 CC not in fibroblasts, endothelial cells or melanocytes. Detected
 CC also in the spleen, brain leukocyte and macrophage cell types.
 CC -1- INDUCTION: By phorbol ester (PMA) and lipopolysaccharide (LPS)
 CC treatment in macrophage cell line.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AF201830; AAF25210.1; -; mRNA.
 CC EMBL: AF186094; AAF02757.1; -; mRNA.
 CC EMBL: AJ242737; CAB59822.1; -; mRNA.
 CC EMBL: AJ242738; CAB59823.1; -; mRNA.
 CC EMBL: A2721338; CAB67704.1; -; Genomic DNA.
 CC EMBL: AF216693; AAF76981.1; -; Genomic DNA.
 CC EMBL: AF230377; AAF91274.1; -; mRNA.
 CC EMBL: BN000002; CAD29877.1; -; Genomic DNA.
 CC EMBL: AY359117; AAO89475.1; -; mRNA.
 CC EMBL: AY972853; AAX59031.1; -; Genomic DNA.
 CC EMBL: AC016724; AAY14990.1; -; Genomic DNA.
 CC EMBL: BC024747; AAH24747.1; -; mRNA.
 CC EMBL: PIR; J07104; J07104.
 CC HSSP: P18510; 11LR.
 CC SWR: O9UBH0; 2-155.
 CC IntAct: O9UBH0; -;
 CC Ensembl: ENSG00000136695; Homo sapiens.
 CC HNC: HNC; HNC; IL1F5.
 CC MIM: 605507; -;
 CC CO: GO:0005157; P.interleukin-1 receptor antagonist activity; TAS.
 CC InterPro: IPR000975; Interleukin 1.
 CC InterPro: IPR003296; Interleukin1A.
 CC InterPro: IPR003297; Interleukin1A.
 CC PANTHER: PTHR10078:SF2; Interleukin1A; 1.
 CC Pfam: PF00340; IL1; 1.
 CC PRINTS: PR00264; INTERLEUKIN1.
 CC PRINTS: PR01359; INTERLEUKIN1B.
 CC PRINTS: PR01360; INTERLEUKIN1X.
 CC ProDom: PD002536; Interleukin_1; 1.
 CC SMART: SM00125; IL1; 1.
 CC PROSITE: PS00253; INTERLEUKIN_1; 1.
 CC Cytokine family; Polymorphism.
 CC Disulfid 8 154 By similarity.
 CC VARIANT 47 47 N -> S.

Query Match 89.6%; Score 734; DB 1; Length 155;
 Best Local Similarity 91.0%; Pred. No. 5.2e-68;
 Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

DB 1 MYSLGALCFRMDKSLKVLVYHNNOLLGAGLHAGVYIKKEEISVVPNRWLDLSLSPVILG 60

QY 2 MYSLGALCFRMDKSLKVLVYHNNOLLGAGLHAGVYIKKEEISVVPNRWLDLSLSPVILG 61

DB 62 VGGGSCQCSGCGVGEFTLTLEPNVIMELTGAKESKSPFYRRDGLTSSPESAAYPGMF 121

QY 61 VGGGSCQCSGCGVGEFTLTLEPNVIMELTGAKESKSPFYRRDGLTSSPESAAYPGMF 120

DB 122 LCTSPEDQVRLTQIPEDPAMDAPITDYPFOCCD 156

QY 121 LCTSPEDQVRLTQIPEDPAMDAPITDYPFOCCD 155

DB 121 LCTSPEDQVRLTQIPEDPAMDAPITDYPFOCCD 155

RESULT 3

OS42M1_MOUSE PRELIMINARY; PRT; 159 AA.

ID OS42M1_MOUSE PRELIMINARY; PRT; 159 AA.

AC OS42M1; 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

DE 0 day neonate skin cDNA, RIKEN full-length enriched library, full

DE clone:4632427H17 product:interleukin 1 receptor antagonist, full

DE insert sequence.

OS Name=il1rn;

GN Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RL 1)

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barth G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima U., Mazzarelli J., Sakamoto N.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Noraki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.,

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Otsu N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schoenbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Coueins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Girmond S., Gustinich S., Hirokawa N., Jackson I.D., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Savelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Vetraro R., Wagner L., Wyszewski-Boris A., Yangisawa M., Yang I., Yang L.,

RA Wilming L.G., Wyszewski-Boris A., Yangisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Arakawa K., Arakawa T., Fukuda I.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.,

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [5]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Arakawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Kono H., Akiyama J., Nishi K., Kitsuana T., Teshiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

RT "RIKEN integrated sequence analysis (RISA) system-384 format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [7]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [8]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [9]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [10]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [11]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [12]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [13]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [14]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [15]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [16]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [17]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

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RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

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RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

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RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [18]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

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RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [19]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

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RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [20]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:0030073; P:insulin secretion; IMP.

DR GO; GO:0006629; P:lipid metabolism; IMP.

RN [21]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Adachi J., Arakawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katon H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi P., Takaku-Akashira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AK076296; BAC36291.1; -, mRNA.

DR MGI; MGI:16547; Il1rn.

DR GO; GO:003007

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QY 10 FRKMSALXLYLHNNOLLAGLHAERKIVGSEISVVPNRALDASLSPVILGVGSSQCL 69
DB 20 FRMDWNTOKFTYLRNNOIAGYLQGPNIKLEBKIDWP-----IDLHSPVFLGHGKCL 74
QY 70 SCGTEKGP1-LKLEPVNIMELYLAKESKSFYFRDMGLTSSPESAAYPGWFLCTSPBA 128
DB 75 SCAGSGDITKQLEEVNITLDSKNKEBDKRTFTFRSEKPTTSPESAACPGWFLCTTLEA 134

QY 129 DQPVRLTQIPEDPAMPADITDFYPOQ 154
DB 135 DRPVSLTNPPEP---LIVTKFYFOE 157

RESULT 4
IL1RA MOUSE
ID IL1RA MOUSE STANDARD; PRT; 178 AA.
AC P25085; 070207;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IRAP)
DE (IL1 inhibitor) (IL-1RN).
GN Name=il1rn; Synonyms=il-1ra;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
(1)
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=91250712; PubMed=1828262;
RA Zahedi K., Seiden M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;
RT "Mouse IL-1 receptor antagonist protein. Molecular characterization,
RT gene mapping, and expression of mRNA in vitro and in vivo.";
RL J. Immunol. 146:4228-4233(1991).
(2)
RN NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=91316273; PubMed=1830498;
RA Matsushima H., Roussel M.F., Matsushima K., Hishinuma A., Sherr C.J.;
RT "Cloning and expression of murine interleukin-1 receptor antagonist in
RT macrophages stimulated by colony-stimulating factor 1.";
RL Blood 78:616-623(1991).
(3)
RN NUCLEOTIDE SEQUENCE (ISOFORM 1).
RP STRAIN=Swiss;
RX MEDLINE=94271931; PubMed=8003626; DOI=10.1016/1043-4666(94)90001-9;
RA Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;
RT "The mouse interleukin-1 receptor antagonist protein: gene structure
RT and regulation in vitro.";
RL Cytokine 6:1-9(1994).
(4)
RN NUCLEOTIDE SEQUENCE (ISOFORM 2).
RP STRAIN=FVB X DBA/1 LACJ;
RX MEDLINE=98209757; PubMed=9550387;
RA Gabay C., Porter B., Fancuzzi G., Arend W.P.;
RT "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning
RT and protein expression of intracellular isoform and tissue
RT distribution of secreted and intracellular IL-1 receptor antagonist in
RT vivo.";
RL J. Immunol. 159:5905-5913(1997).
(5)
RN NUCLEOTIDE SEQUENCE OF 7-178.
RP MEDLINE=91271363; PubMed=1828896;
RX Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA Brandhuber B.J., Thompson R.C.;
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT gene family: evolution of a cytokine control mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
(6)
RN NUCLEOTIDE SEQUENCE OF 23-178.
RP MEDLINE=92037824; PubMed=1834470;
RX Shuck M.E., Bessau T.E., Tracey D.E., Bienkowiak M.J.;
RT "Cloning, heterologous expression and characterization of murine

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RT Interleukin 1 receptor antagonist protein.";
RL Eur. J. Immunol. 21:2775-2780(1991).
CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
CC receptor. Has no IL-1 like activity.
CC -1- SUBCELLULAR LOCATION: Secreted (isoform 1). Cytoplasmic (isoform
CC 2).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P25085-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P25085-2; Sequence=VSP_002652;
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC
CC This Swiss-Prot entry is copyrigh. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M74294; AAA9309.1; -; mRNA.
CC EMBL; M64404; AAA9277.1; -; mRNA.
CC EMBL; U32838; AAA30576.1; -; Genomic_DNA.
CC EMBL; AF001795; AAC15251.1; -; mRNA.
CC EMBL; M57525; AAA9278.1; -; mRNA.
CC EMBL; M63100; AAA9310.1; -; Genomic_DNA.
CC EMBL; S64082; AAB20265.1; -; mRNA.
CC PIR; A44610; A44610.
CC HSSP; P18510; 11RA.
CC SMR; P25085; 35-178.
CC EMBL; ENSMUSG0000026981; Mus musculus.
CC MGI; MGI:96547; 11rn.
CC GO; GO:0030073; P:insulin secretion; IMP.
CC GO; GO:0006629; P:lipid metabolism; IMP.
CC InterPro; IPR000975; Interleukin_1.
CC InterPro; IPR003286; InterleukinIL1B.
CC InterPro; IPR003287; InterleukinIL1RA.
CC PANTHER; PTHR10078:SP2; InterleukinIL1RA; 1.
CC Pfam; PF00340; IL1; 1.
CC PRINTS; PR00264; INTERLEUKIN1.
CC PRINTS; PR01359; INTERLEUKIN1B.
CC PRINTS; PR01360; INTERLEUKIN1X.
CC PRODOM; PD002536; Interleukin_1; 1.
CC PROSITE; PS00253; INTERLEUKIN_1; 1.
CC KMW Alternative splicing; Glycoprotein; Signal.
CC SIGNAL 1 26 By similarity.
CC CHAIN 27 178 Interleukin-1 receptor antagonist
CC protein.
CC CARBOHYD 110 110 N-linked (GlcNAc...) (potential).
CC DISULFID 92 142 By similarity.
CC VARSPLIC 1 21 MEICWGPSYSHISLILILFFH -> MA (in isoform
CC 2).
SQ SEQUENCE 178 AA; 20274 MW; 84AA002A119C024 CRC64;
Query Match 39.0%; Score 319.5; DB 1; Length 178;
Best Local Similarity 48.6%; Pred. No. 8e-25;
Matches 71; Conservative 17; Mismatches 49; Indels 9; Gaps 3;

QY 10 FRKMSALXLYLHNNOLLAGLHAERKIVGSEISVVPNRALDASLSPVILGVGSSQCL 69
DB 39 FRMDWNTOKFTYLRNNOIAGYLQGPNIKLEBKIDWP-----IDLHSPVFLGHGKCL 93
QY 70 SCGTEKGP1-LKLEPVNIMELYLAKESKSFYFRDMGLTSSPESAAYPGWFLCTSPBA 128
DB 94 SCAGSGDITKQLEEVNITLDSKNKEBDKRTFTFRSEKPTTSPESAACPGWFLCTTLEA 153
QY 129 DQPVRLTQIPEDPAMPADITDFYPOQ 154
DB 154 DRPVSLTNPPEP---LIVTKFYFOE 176

RESULT 5

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ID	Accession	Species	Gene	Length (bp)	Source	Notes
0542C7	MOUSE	PRELIMINARY				
AC	0542C7					
DT	13-SEP-2005	(TREMBL)	31	Last sequence update		
DT	13-SEP-2005	(TREMBL)	31	Last annotation update		
DT	13-SEP-2005	(TREMBL)	31	Last annotation update		
DE	NOD-derived	CD1c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:FE30041P17 product:interleukin 1 receptor antagonist,				
DE	full insert sequence.					
GN	Name:Il1rn					
OS	Mus musculus (Mouse)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;					
OC	Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=MOD;					
RC	MEDLINE=929729253; PubMed=10349636; DOI=10.1016/S0076-6876(99)03004-9;					
RA	Carninci P., Hayashizaki Y.;					
RT	"High-efficiency full-length cDNA cloning.";					
RL	Meth. Enzymol. 303:19-44(1999).					
RP	[2]					
RN	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=MOD;					
RC	MEDLINE=22355683; PubMed=12117851; DOI=10.1038/35055500;					
RA	Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,					
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,					
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,					
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,					
RA	Kadoya K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,					
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,					
RA	Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,					
RA	Schirral L. M., Staudt F., Suzuki R., Tomita M., Wagner L., Weng G.,					
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barin G.,					
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,					
RA	Bromberg M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,					
RA	Guernicich S., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N. H.,					
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaefts P.,					
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,					
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,					
RA	Suzuki H., Toyooka K., Wang K. H., Welter C., Whitaker C., Wilming L.,					
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J. H., Kohetsuki S.,					
RA	Hayashizaki Y.;					
RT	"Functional annotation of a full-length mouse cDNA collection.";					
RL	Nature 409:685-690(2001).					
RP	[3]					
RN	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=MOD;					
RC	MEDLINE=22355683; PubMed=12466851; DOI=10.1038/nature01266;					
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,					
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamana K. I., Kiyosawa H.,					
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schenbach C., Gojobori T.,					
RA	Baldarelli R., Hill D. P., Bult C., Hume D. A., Quackenbush J.,					
RA	Schirral L. M., Knapin A., Matsuda H., Batalov S., Bessel K. M.,					
RA	Blake J. A., Brad D., Busic V., Chochia C., Corbini L. E., Cousins S.,					
RA	Dalla E., Dragan T. A., Fletcher C. F., Forrest A., Frazier K. S.,					
RA	Gaasterland T., Gariboldi M., Gissi C., Godik A., Gough J.,					
RA	Griffond S., Guernicich S., Hirokawa N., Jackson I. J., Jarvis E. D.,					
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzierski R. M., King B. A.,					
RA	Kongawa A., Kurochkin I. V., Lee Y., Lennard B., Lyons P. A.,					
RA	Maglott D. R., Maltais L., Marchionni L., McKenzie L., Miki H.,					
RA	Nagashima T., Numata K., Okido T., Pavan W. J., Petrea G., Pesole G.,					
RA	Petrovsky N., Pillai R., Pontius J. V., Qi D., Ramachandran S.,					
RA	Ravasi T., Reed J. C., Reed D. J., Reid J., Ring B. Z., Ringwald M.,					
RA	Sandelin A., Schneider C., Sempé C. A., Seton M., Shimada K.,					
RA	Sultana R., Takemura Y., Taylor M. S., Tesdale R. D., Tomita M.,					
RA	Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,					
RA	Wilming L. G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,					
RA	Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,					
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,					
RA	Ishizaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,					
RA	Hara A., Hashizume W., Imotani K., Ish					

RA	Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA	Yaenishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA	Birney E., Hayashizaki Y. ;
RT	"Analysis of the mouse transcriptome based on functional annotation of
RT	60,770 full-length cDNAs." ;
RL	Nature 420:563-573(2002).
RN	[4]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=NDJ;
RC	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RX	Shibata K., Itoh M., Aizawa K., Nagoka S., Sasaki N., Carninci P.,
RA	Komori H., Akiyama J., Nishi K., Kitsumi T., Tashtiro H., Itoh M.,
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwaagi K.,
RA	Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawal J.,
RA	Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y. ;
RT	"Riken integrated sequence analysis (RISA) system-384-format
RT	sequencing pipeline with 384 multicapillary sequencer." ;
RL	Genome Res. 10:1757-1771(2000).
RN	[6]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=MOD;
RC	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA	Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA	Hayashida K., Hayatsu N., Hiramoto K., Hiroka T., Hirokawa T.,
RA	Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA	Kato H., Kawal J., Koijima Y., Kondo S., Komori H., Koya S.,
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA	Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA	Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA	Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA	Tegawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA	Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y. ;
RL	Submitted (APR-2002) to the EMBL/genbank/DBD databases.
DR	EMBL: AK089222; BAC04079.1; -; mRNA.
DR	MGI: MG1:96547; Ilrn.
DR	GO: GO:0030073; p:insulin secretion; IMP.
DR	GO: GO:0006629; p:lipid metabolism; IMP.
KW	Receptor.
SO	SEQUENCE 178 AA; 20274 MW; 84AA02NA31J9C024 CRC64;
QY	Query Match 39.0%; Score 319.5; DB 2; Length 178;
Db	Best Local Similarity 48.6%; Pred. No. 8e-25;
Matches	71; Conservative 17; Mismatches 49; Indels 9; Gaps 3
QY	10 FRMKDSALXYLYLNHNOGLAGSLHAELVKGSEISIVPRNALDAASLVILGVGGSSQL 69
Db	39 FRIMDTMOKFYLLNNOLINGYLQGPVIKLEKKIDWP-----IDLHSVFLGHHGKCL 93
QY	70 SCGTKEKPI-LKPEPVIMELYGAESKSFTFYRRDMGLTSPFESAAYVGFCTSPFA 128
Db	94 SCASGDIKIQLAEVAVITDLSKNKEDKFTPIRSKGTTFPESAACGWFLCTLLEA 153
QY	129 DOVRLTIQIPDPAMDAPTDFYFOO 154
Db	154 DRPSLTNTPEEP---LIIVTFYFOE 176
RESULT 6	
OGCGAI_MOUSE PRELIMINARY; PRJ; 159 AA.	
OGCGAI; AC 01-MAR-2003 (TrEMBLrel. 23, Created)	

DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
DE Interleukin 1 receptor antagonist.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N.
RC TISSUE=Mammary tumor. Metallotionien-TGF alpha model. 10 month old
RC Virgin mouse. Taken by biopsy.
RX MEDLINE=2338825; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Stachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebli T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lomellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gutierrez P.H.,
RA Richards D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Scherch J.B., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N.
RC TISSUE=Mammary tumor. Metallotionien-TGF alpha model. 10 month old
RC Virgin mouse. Taken by biopsy.
RL Strausberg R.;
EMBL: BC042532; AHA42532.1; -, mRNA.
DR HSSP: P18510; 11LR.
DR SMR: Q8CGA1; 16-159.
DR MGI: 96547; 11lrn.
DR GO: 0030073; P: insulin secretion; IMP.
DR GO: 0006629; P: lipid metabolism; IMP.
DR InterPro: IPR003294; InterleukinIL1B.
DR InterPro: IPR003296; InterleukinIL1B.
DR InterPro: IPR003297; InterleukinIL1B.
DR InterPro: IPR000975; InterleukinIL1RA.
DR Pfam: PF00340; IL1; 1.
DR PRINTS: PR00264; INTERLEUKIN1.
DR PRINTS: PR01359; INTERLEUKIN1B.
DR PRINTS: PR01360; INTERLEUKIN1X.
DR PRINTS: PR01357; INTERLEUKIN1AB.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
KW Receptor.
SQ SEQUENCE 159 AA; 17995 MW; BCA081C172903367 CRC64;
Query Match 38.8%; Score 317.5; DB 2; Length 159;
Best Local Similarity 47.9%; Pred. No. 1, 1e-24;
Matches 70; Conservative 18; Mismatches 49; Indels 9; Gaps 3;
QY 10 FFMKDSALVLYLHNNQLAGGLHAKEVKIGBEISVPPNRALDASISPVILGVGGSGCL 69
DB 20 FFLMIDNQKTFYLRNNQLAGVLYQGPNIKLEKLDVDP-----IDLHSAFLGIHGKCL 74
QY 70 SCGTGKGPL-LKLEFPVNIWELVYGAKESSFTFYRRDMGLTSFESAAAPGWLCTSPRA 128

DB 75 SCAGSDDIKLQLEENITDLSKKEEDKRFPIINSEKPTTSFESACPGWFLCTTLEA 134
QY 129 DQPVRLTQIPBDPAMDAPITDFYFQ 154
DB 135 DRPVSLTNTRPEP---LIVTKFYFQE 157
RESULT 7
ID IL1FA MOUSE STANDARD; PRT; 152 AA.
AC 08R459;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin 1 family member 10 (IL-1F10).
GN Name=IL1F10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Swiss Webster / NIH;
RX MEDLINE=21988051; PubMed=11991723; DOI=10.1006/geno.2002.6752;
RX Taylor S.L., Renshaw B.R., Garika K.E., Smith D.E., Sims J.E.,
RT "Genomic organization of the interleukin-1 locus.";
RL Genomics 79:726-733(2002).
CC -1- FUNCTION: Binds soluble IL-1 receptor type 1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (by similarity).
CC -1- SIMILARITY: Belongs to the IL-1 family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL: AY071844; AAL67155.1; -, mRNA.
DR HSSP: P18510; 11RA.
DR Ensemble: ENSMUSG0000046845; Mus musculus.
DR MGI: 2652548; 11f10.
DR InterPro: IPR000975; Interleukin_1.
DR InterPro: IPR003296; InterleukinIL1B.
DR InterPro: IPR003297; InterleukinIL1RA.
DR PANTHER: PTHR10078:SP2; InterleukinIL1RA; 1.
DR Pfam: PF00340; IL1; 1.
DR PRINTS: PR00264; INTERLEUKIN1.
DR PRINTS: PR01359; INTERLEUKIN1B.
DR PRINTS: PR01360; INTERLEUKIN1X.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; FALSE_NBG.
KW Cytokine; Multigene family.
SQ SEQUENCE 152 AA; 17078 MW; 9AD03BB0C361D8A CRC64;
Query Match 38.1%; Score 312; DB 1; Length 152;
Best Local Similarity 43.5%; Pred. No. 4e-24;
Matches 67; Conservative 28; Mismatches 53; Indels 6; Gaps 3;
QY 1 MMTLSGALCFRMKDSALVLYLHNNQLAGGLHAKEVKIGBEISVPPNRALDASISPVIL 60
DB 1 MCSLPMARYYIIKDHQKALYTRNQQLIGPDSDN-YSPEKVCILPKNGLDRSKVPYFL 59
QY 61 GVGGSGGCLSC-GTEKGPLIKLEFPVNIWELVYGAKESSFTFYRRDMGLTSFESAAAPG 119
DB 60 GMGGSSCCLACVKTREGPLQLEEDVNIIDLTKGGEQTRFTFQNSLDSAPFLHAAACPG 119
QY 120 WFLCTSPADQPVRLTQIPBDPAMDAPITDFYFQ 153
DB 120 WFLGPAEPQGPVQVLTKESE---PSTHTETFEF 149

RESULT 8
 Q56AT8 HUMAN PRELIMINARY; PRT; 152 AA.
 ID 056AT8;
 AC 056AT8;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Interleukin 1 family, member 10 (Theta).
 GN Name=IL1F10;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Rieder M.J., Johanson E.J., da Ponte S.H., Haastings N.C., Ahern M.O.,
 RA Bettucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY972854; AAK59032.1; -; Genomic DNA.
 SQ SEQUENCE 152 AA; 16975 MW; DF973510FC711B2 CRC64;
 Query March 37.7%; Score 309; DB 2; Length 152;
 Best Local Similarity 45.2%; Pred. No. 8.1e-24;
 Matches 70; Conservative 23; Mismatches 56; Indels 6; Gaps 3;
 QY 1 MMVLSGALCFRMKDSALKVLYLHNNQLAGLHAERVKGEISIVVPRALDASLPYL 60
 DB 1 MSLIMARYIIRKVDQKALYTRDGLVGDPAVNCC-AEKICTLPNKGIDRTKVPITL 59
 QY 61 GVQGSQCLSC-GTEGPKLKLKPVNIMELYGAKESFTFYRRDMGLTSSFESAAYPG 119
 DB 60 GIGQSGRCACVETGSPSLQEDVITIELYKGEATFTFFQSSGSAFRLKAAMPG 119
 QY 120 WFLCTSPBADQVRLTQIPEDPMDAPITDFYFQQ 154
 DB 120 WFLCGAPFPQPVQQLTKESPSA----RTKVFYEQ 150
 RESULT 9
 IL1RA HUMAN STANDARD; PRT; 177 AA.
 ID IL1RA HUMAN;
 AC P18510; Q14628; Q7RTZ4; Q96GP6; Q9UPC0;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IRAP)
 DE (IL1 inhibitor) (IL-1RN) (ICIL-1RA).
 GN Name=IL1RN; Synonyms=IL1F3, IL1RA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RX MEDLINE=90220867; PubMed=2139180; DOI=10.1038/344633a0;
 RA Carter D.B., Deibel M.R., Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
 RA Slighcom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwen R.N.,
 RA Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Siu L.C.,
 RA Hardee M.M., Zurcher-Nelly H.A., Reardon I.M., Heinrichson R.L.,
 RA Truesdell S.E., Shelly J.A., Bessalu T.E., Taylor B.M., Tracey D.E.;
 RA "Purification, cloning, expression and biological characterization of
 RA an interleukin-1 receptor antagonist protein."
 RT Nature 344:633-638 (1990).
 RL [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RX MEDLINE=90136921; PubMed=2137201; DOI=10.1038/343341a0;
 RA Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,
 RA Hannum C.H., Thompson R.C.;
 RA "Primary structure and functional expression from complementary DNA of
 RA a human interleukin-1 receptor antagonist."
 RL Nature 343:341-346 (1990).

[3]
 RN NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RX MEDLINE=91271363; PubMed=1828896;
 RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
 RA Brandhuber B.J., Thompson R.C.;
 RT Interleukin 1 receptor antagonist is a member of the interleukin 1
 RT gene family: evolution of a cytokine control mechanism."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236 (1991).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RX MEDLINE=92338323; PubMed=1385987; DOI=10.1016/1043-4666(92)90041-O;
 RA Leonard A., Gorman P., Carrier M., Griffiths S., Scotney H., Sheer D.,
 RA Solari R.;
 RA "Cloning and chromosome mapping of the human interleukin-1 receptor
 RT antagonist gene."
 RL Cytokine 4:83-89 (1992).
 RN [5]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 3).
 RX MEDLINE=97146044; PubMed=892991;
 RA Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slighcom J.L.,
 RA Arend W.P., Smith M.F., Jr.;
 RA "Intracellular IL-1 receptor antagonist promoter: cell type-specific
 RT and inducible regulatory regions."
 RL J. Immunol. 158:748-755 (1997).
 RN [6]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
 RX MEDLINE=91219436; PubMed=1827201;
 RA Haekil S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,
 RA Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
 RT "cDNA cloning of an intracellular form of the human interleukin 1
 RT receptor antagonist associated with epithelium."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685 (1991).
 RN [7]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 3).
 RX MEDLINE=9535865; PubMed=7629520; DOI=10.1084/jem.182.2.623;
 RA Muzio M., Polentarutti N., Sironi M., Poli G., De Giola L.,
 RA Introna M., Mantovani A., Colotta F.;
 RT "Cloning and characterization of a new isoform of the interleukin 1
 RT receptor antagonist."
 RL J. Exp. Med. 182:623-628 (1995).
 RN [8]
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
 RA Rieder M.J., Carrington D.P., Haastings N.C., Ahern M.O.,
 RA Kulander S.A., Rajkumar N., Toth B.J., Yi Q., Nickerson D.A.;
 RT "SeattlesNBS, NHBLI HL6682 program for genomic applications, UW-
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>)."
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM 2).
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldi M.P., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udén T.B., Toehyink S., Carninci P., Pirange C.,
 RA Rask S.S., Loguella N.A., Peters G.J., Malek J.A., Gnaratne P.H.,
 RA Bobak S.A., McKean P.J., McKernan K.J., Alek J.A., Luyk S.W.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
 RA Villalón D.K., Muzny D.M., Sodegren E.J., Lu X., Gibbs R.A.,
 RA Valley J., Hailon E., Keltman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Schmutz J., Myers R.M.,
 RA Rodriguez A.C., Grimwood J., Skalska U., Smallus D.E.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.B., Jones S.J.W., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [10]
 RP PROTEIN SEQUENCE OF 26-45, AND CARBOHYDRATE-LINKAGE SITE ASN-109.

RX MEDLINE=90136920; Pubmed=2137200; DOI=10.1038/343336a0;
 RA Hannum C.H., Wilcox C.J., Arand W.P., Joslin F.G., Dixups D.J.,
 RA Helmdel P.L., Ames L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
 RT "Interleukin-1 receptor antagonist activity of a human interleukin-1
 RT inhibitor.";
 RL Nature 343:336-340(1990).
 RN [11]
 RP PROTEIN SEQUENCE OF 26-52
 RX MEDLINE=90354444; Pubmed=2143761;
 RA Blenkowski M.J., Baessau T.E., Berger A.E., Truesdell S.E.,
 RA Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
 RA Heriksson R.L., Chosey J.G., Tracey D.E.;
 RT "Purification and characterization of interleukin 1 receptor level
 RT antagonist proteins from THP-1 cells.";
 RL J. Biol. Chem. 265:14505-14511(1990).
 RN [12]
 RP NUCLEOTIDE SEQUENCE OF 35-177 (ISOFORM 4).
 RX MEDLINE=98183404; Pubmed=9518484; DOI=10.1006/bdrc.1998.8217;
 RA Welsbach L., Tran K., Colquhoun S.A., Champiand M.F., Towle C.A.;
 RT "Detection of an interleukin-1 intracellular receptor antagonist mRNA
 RT variant.";
 RL Biochem. Biophys. Res. Commun. 244:91-95(1998).
 RN [13]
 RP IDENTIFICATION OF ISOFORM 2.
 RX MEDLINE=21988050; Pubmed=11991722; DOI=10.1006/geno.2002.6751;
 RA Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald W.G., Duff W.G.,
 RA Korzman K.;
 RT "A sequence-based map of the nine genes of the human interleukin-1
 RT cluster.";
 RL Genomics 79:718-725(2002).
 RN [14]
 RP STRUCTURE BY NMR.
 RX MEDLINE=92297633; Pubmed=1534997;
 RA Stockman B.U., Scallill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
 RA Brunner D.P., Yem A.W., Deibel M.R. Jr.;
 RT "Secondary structure and topology of interleukin-1 receptor antagonist
 RT protein determined by heteronuclear three-dimensional NMR
 RT spectroscopy.";
 RL Biochemistry 31:5237-5244(1992).
 RN [15]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94320651; Pubmed=8045306; DOI=10.1016/0014-5793(94)00643-1;
 RA Stockman B.U., Scallill T.A., Strakalaitis N.A., Brunner D.P.,
 RA Yem A.W., Deibel M.R. Jr.;
 RT "Solution structure of human interleukin-1 receptor antagonist
 RT protein.";
 RL FEBS Lett. 349:79-83(1994).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=94230368; Pubmed=8175703;
 RA Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,
 RA Brandhuber B.J.;
 RT "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
 RT resolution.";
 RL J. Biol. Chem. 269:12874-12879(1994).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=95172072; Pubmed=7867645;
 RA Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E.,
 RA Akesson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
 RT "Refined crystal structure of the interleukin-1 receptor antagonist.
 RT Presence of a disulfide link and a cis-proline.";
 RL Eur. J. Biochem. 227:838-847(1995).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
 RX MEDLINE=97215904; Pubmed=9062194;
 RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A., Sarubbi E.,
 RA Sarubbi E., Akesson A., Bowlin T., Yanofsky S., Barrett R.W.;
 RT "Structure of the interleukin-1 receptor binding mode revealed by the crystal
 RT structure of the IL-1 receptor with an antagonist.";
 RL Nature 386:194-200(1997).
 CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
 receptor. Has no IL-1 like activity.

```

CC -1- SUBCELLULAR LOCATION: Secreted (Isoform 1). Cytoplasmic (Isoforms
CC 2, 3 and 4).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC Isoform=1; Sequence=Displayed;
CC Name=2; Synonyms=ICIL-1ra;
CC Isoform=1; Sequence=VSP_002649;
CC Name=3; Synonyms=ICIL-1ra type II;
CC Isoform=1; Sequence=VSP_002650;
CC Name=4;
CC Isoform=1; Sequence=VSP_002651;
CC -1- TISSUE SPECIFICITY: The intracellular form of IL1RN is
CC predominantly expressed in epithelial cells.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -1- DATABASE: NMR-RD Systems' cyclohex source book: IL1RN;
CC WWW="http://www.ridsystems.com/asp/g_sbuilder.asp?bodyid=205".
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation --
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC
Qy Query Match 37.5%; Score 307.5; DB 1; Length 177;
Best Local Similarity 48.0%; Pred. No. 1.4e-23;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;
Db 10 FRKDSALKVLVLIHNNQLAGLHAERVIKGEISVVPNALDASLP--VILGVGGSGQ 67
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
38 FRIDVNVQKFFYLRNNQVLVAGVLGQRPVNLBKIDVP-----IFPALFGIHGKM 90
Qy 68 CLSC--GTEKGPIKLEPYNIMELVIGAKSSFTFRYDMGLTSSFSANIPGFILCT 124
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 91 CLSCVKSQSDETR--LQLEAVNITDLSNRKQDRFAFRSDSGPTSPFSAACPGFELCT 148
Qy 125 SPKADQPVRLTQIPEDPAMDAPITDPFPOQ 154
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Db 149 AMEADQPVSLINMPDR--GVMTKTFYQK 175
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ID 053SC2_HUMAN PRELIMINARY; PRT; 180 AA.
AC 053SC2;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein IL1RN.
GN Name=IL1RN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP Scott K., Doeber A., Mailey B.;
RP "The sequence of Homo sapiens BAC clone RP11-97J14.";
RP Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RP Waterston R.H.;
RP Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RP Waterston R.;
RP Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RP Wilson R.K.;
RP Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RN EMBL; AC024704; AA933278.1; --; Genomic_DNA.
RW Hypothetical protein.

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QY 10 FMKDSALKVLYHNNQIAGLHAERKVIKGEISVFNRLDASLSP--VILGVGGSG 67
 DB 38 FRIWVNOCKTFYLRNNQIAGVAGYLOGENTKLEEKIDVVP-----IEPAMFLGIHGK 90
 QY 68 CISCCTGKCPILK--LEPNIMELVYGAESKSFYTRDMLTSSFESAIPGWLCTS 125
 DB 91 CIAC-VKSGDEIKLGLPEPNITDLSNKKEDKRFARIRSDSGPTTSFESACPGWFLCTA 149
 QY 126 PEADQVRLTQIPEPAMDAPITDFYFQQ 154
 DB 150 LETDQVGLTNTPPQDA---VQYTKFYFQQ 175
 RESULT 13
 IL1FA HUMAN
 ID IL1FA HUMAN STANDARD: PRT; 152 AA.
 AC Q8MWZ1; Q7RTZ5; Q969H5; Q9BX11;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 13-SEP-2003 (Rel. 48, Last sequence update)
 DT 13-SEP-2003 (Rel. 48, Last annotation update)
 DE Interleukin 1 family member 10 (IL-1F10) (Interleukin-1 receptor
 antagonist-like FcR1 theta (Interleukin-1 theta) (IL-1 theta) (F1L1
 theta) (Interleukin-1 HT2) (IL-1HT2).
 GN Name=IL1F10; Synonyms=F1L1T, IL1HT2;
 ORNames=FKSG75, UNOC6119/PRO20041;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Carnivora; Homi
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RC TISSUE=Thymus;
 RX MEDLINE=21615180; PubMed=11747621; DOI=10.1089/107999001753289505;
 RA Benen J.T., Dawson P.A., Mychaleckyj J.C., Bowden D.W.;
 RT "Identification of a novel human cytokine gene in the interleukin
 RT cluster on chromosome 2q12-14.";
 RL J. Interferon Cytokine Res. 21:899-904 (2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
 RA Wang Y.-G., Li T., Gong L.;
 RT "Identification and characterization of FKSG75, a novel member of the
 RT interleukin-1 family.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA / mRNA) (ISOFORM 1), AND VARIANTS
 RP THR-44 AND ASP-51.
 RC TISSUE=Fetal skin;
 RX MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
 RA Lin H., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussell J.,
 RA Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
 RT "Cloning and characterization of IL1HT2, a novel interleukin-1 family
 RT member.";
 RL J. Biol. Chem. 276:20597-20602 (2001).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
 RX MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
 RA Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
 RA Kornman K.;
 RT "A sequence-based map of the nine genes of the human interleukin-1
 RT cluster.";
 RL Genomics 79:718-725 (2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM 1).
 RX MEDLINE=22887296; PubMed=12973509; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Adaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heidens S.,
 RA Huang A., Kim H.S., Klimowaki L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Sehnaghi S., Simone L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R.L., Watanabe C., Wleand D., Woode K., Xie M.-H.,

RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270 (2003).
 RN [6]
 RP VARIANTS THR-44 AND ASP-51.
 RX MEDLINE=21988051; PubMed=11991723; DOI=10.1006/geno.2002.6752;
 RA Taylor S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E.;
 RT "Genomic organization of the interleukin-1 locus.";
 RL Genomics 79:726-733 (2002).
 CC -1- FUNCTION: Binds soluble IL-1 receptor type 1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8MWZ1-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8MWZ1-2; Sequence=VSP_002658;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Expressed in fetal skin, spleen and tonsil.
 CC Expressed mostly in the basal epithelia of skin and in
 CC proliferating B cells of the tonsil.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AY029413; AAK33010.1; -; mRNA.
 DR EMBL; AY026753; AAK01948.1; -; mRNA.
 DR EMBL; AF334755; AAK68048.1; -; mRNA.
 DR EMBL; AF334756; AAK68049.1; -; Genomic DNA.
 DR EMBL; BN000002; CAD29878.1; -; Genomic DNA.
 DR EMBL; AY358846; AAO89205.1; -; mRNA.
 DR HSSP; P18510; IL1R.
 DR Ensembl; ENSG00000136697; Homo sapiens.
 DR HGNC; HGNC:1552; IL1F10.
 DR InterPro; IPR000975; Interleukin_1.
 DR InterPro; IPR003296; InterleukinF1b.
 DR InterPro; IPR003297; InterleukinIL1b.
 DR PANTHER; PTHR10078:SF2; InterleukinIL1b; 1.
 DR Pfam; PF00340; IL1; 1.
 DR PRINTS; PRO0264; INTERLEUKIN1.
 DR PRINTS; PRO1359; INTERLEUKIN1B.
 DR PRINTS; PRO1360; INTERLEUKIN1X.
 DR PRODOM; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; FALSE NEG.
 KM Alternative splicing; Cytokine, Multigene family, Polymorphism.
 FT VARSPLIC 9
 FT YIYIKYADQKLYTRDQGLVDDVADNCA -> MSSSPL
 FT PEPAPSLQHGVLSDSSLSL (in isoform 2).
 FT /FTid=VSP_002658.
 FT VARIANT 44 44 I -> T (in dbSNP: 6761276).
 FT /FTid=VAR_014262.
 FT VARIANT 51 51 A -> D (in dbSNP: 6743376).
 FT /FTid=VAR_014263.
 SQ SEQUENCE 152 AA; 16943 MW; E0ABD2496551B34F CRC64;
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 Best Local Similarity 44.5%; Pred. No. 2,7e-23;
 Matches 69; Conservative 24; Mismatches 56; Indels 6; Gaps 3;
 QY 1 MMTVSGALCFRMKDSALKVLYHNNQIAGLHAERKVIKGEISVFNRLDASLSPYL 60
 DB 1 MCSLPMARYIYIKYADQKLYTRDQGLVDDVADNCC-BKIKCILPFRGIARFVIFL 59
 QY 61 GVGCGSGCASC-GTEKCPILKLEPNVIMELVYGAESKSFYTRDMLTSSFESAAYPG 119
 DB 60 GIGGSGRCLACVETBSPSLQLEVDNIEILYKGEISVFNRLDASLSPYL 119

QY 120 WFLCTSPADQPVRLTQIPEDPAMDAPITDFYFOO 154
 Db 120 WFLCGPAEPQOPVOLTKESEPSA-----RTKFFYFQ 150

RESULT 14

Q53SR9 HUMAN PRELIMINARY; PRT; 152 AA.
 AC Q53SR9;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein IL1F10.
 GN Name=IL1F10;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OC NCBI_Taxid=9606;
 OX (1)
 RN NUCLEOTIDE SEQUENCE.
 RA Armstrong J., Haekenson W.;
 RT "The sequence of Homo sapiens BAC clone RP11-339F22.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RN NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RN NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RN NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC016724; AA14991.1; -; Genomic DNA.
 KW Hypothetical protein.
 SO SEQUENCE 152 AA; 16943 MW; E0ABD2496551B34F CRC64;

Query Match 37.1%; Score 304; DB 2; Length 152;
 Best Local Similarity 44.5%; Pred. No. 2.7e-23;
 Matches 69; Conservative 24; Mismatches 56; Indels 6; Gaps 3;

QY 1 MMTLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEKYSVFNRLADSLSPVIL 60
 Db 1 MCGSLPMARYIYIKVADQKALYTRDGLVGPVADNCC-AKICILPNRGLARTKVPFL 59
 QY 61 GVGGSGSCISC-GTEKGPILKLEPVNIMELYLAKESKSPFFYRDMGLTSSPESAAVPG 119
 Db 60 GIGGSSRCCLACVETEEGSGLOLEVDVNEELTKGSEKATRTFFQSSSSGARLDAAMPG 119
 QY 120 WFLCTSPADQPVRLTQIPEDPAMDAPITDFYFOO 154
 Db 120 WFLCGPAEPQOPVOLTKESEPSA-----RTKFFYFQ 150

RESULT 15

IL1RA BOVIN STANDARD; PRT; 174 AA.
 AC 077482;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IRAP)
 DE (IL1 inhibitor) (IL-1RN).
 GN Name=IL1RN;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_Taxid=9913;

RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98305607; PubMed=9643454; DOI=10.1016/S0165-2427(98)00099-3;
 RA Kiritawa R., Fukuda T., Yamana H., Hagiwara K., Goto M., Obata Y.,
 RA Yoshino T., Iwai H.;
 RT "Enzymatic amplification and expression of bovine Interleukin-1
 receptor antagonist cDNA.";
 RL vec. Immunol. Immunopathol. 62:197-208(1998).
 CC -1- FUNCTION: Inhibits the activity of IL-1 by binding to its
 receptor. Has no IL-1 like activity.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

DR EMBL: AB005148; BAA31854.1; -; mRNA.
 DR HSSP: P18510; IL1R.
 DR SMR: O77482; 32-174.
 DR InterPro: IPR000975; Interleukin_1.
 DR InterPro: IPR003297; Interleukin_IL1RA.
 DR PANTHER: PTHR10078:SF2; InterleukinIL1RA; 1.
 DR Pfam: PF00340; IL1; 1.
 DR PRINTS: PR00264; INTERLEUKIN1.
 DR PROSITE: PRO1360; INTERLEUKIN1X.
 DR ProDom: PD002536; Interleukin_1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 KW Glycoprotein; Signal.
 FT SIGNAL 1 23 By similarity.
 FT CHAIN 24 174 Interleukin-1 receptor antagonist
 FT CARBOHYD 107 107 N-linked (GlcNAc...) (Potential).
 FT DISULFID 89 139 By similarity.
 SO SEQUENCE 174 AA; 19926 MW; 1E56E7F224F851F CRC64;

Query Match 36.8%; Score 301.5; DB 1; Length 174;
 Best Local Similarity 48.0%; Pred. No. 5.8e-23;
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 Db 36 FRIMDVNQKIFLIRNNQLVAGVLOGPNTGLBEKIDVP-----IEPTMFLGHGGL 88
 QY 68 CLSCGTEKGPILKLEPVNIMELYLAKESKSPFFYRDMGLTSSPESAAVPGMFLCTSP 126
 Db 89 CLACVSGDEIKLKEAVNITDLMONREDDKPAFIRFNGPTTSPESAAVPGMFLCTSL 148
 QY 127 EADQPVRLTQIPEDPAMDAPITDFYFOO 154
 Db 149 EADQPVGLTMTPEA--LKVTKFFYFOO 173

Search completed: April 5, 2006, 15:12:39
 Job time : 231 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:06:37 ; Search time 26 Seconds

(without alignments)
496.054 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 819
Sequence: 1 MMTLSGALCFRMDKSAKVL.....IPEDPAMDAPITDFFPOCD 156

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Issued Patents AA:*
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3: /cgn2_6/ptodata/1/aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/aa/PTCUS_COMB.pep:*
5: /cgn2_6/ptodata/1/aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	819	100.0	156	2	US-09-398-412B-13
2	809	98.8	154	2	US-09-775-046-11
3	734	89.6	155	2	US-09-417-455-5
4	734	89.6	155	2	US-09-348-942-5
5	734	89.6	155	2	US-09-316-081-5
6	734	89.6	155	2	US-09-578-458-5
7	734	89.6	155	2	US-09-522-964A-5
8	734	89.6	155	2	US-09-457-626-5
9	734	89.6	155	2	US-09-576-008-5
10	734	89.6	155	2	US-09-949-016-6827
11	734	89.6	155	2	US-09-775-046-2
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21	312.5	38.2	178	2	US-09-000-630C-21
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28	309	37.7	169	2	US-09-578-458-4	Sequence 4, Appl1
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32	307.5	37.5	147	2	US-09-775-046-7	Sequence 7, Appl1
33	307.5	37.5	153	2	US-08-796-414-2	Sequence 2, Appl1
34	307.5	37.5	153	2	US-09-131-247-2	Sequence 2, Appl1
35	307.5	37.5	153	2	US-09-131-247-4	Sequence 4, Appl1
36	307.5	37.5	153	2	US-09-784-623-2	Sequence 2, Appl1
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39	307.5	37.5	156	1	US-08-910-733-10	Sequence 10, Appl1
40	307.5	37.5	156	1	US-08-910-884-10	Sequence 10, Appl1
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43	307.5	37.5	159	1	US-08-459-092-2	Sequence 2, Appl1
44	307.5	37.5	159	1	US-08-459-814-2	Sequence 2, Appl1
45	307.5	37.5	159	1	US-08-425-232-2	Sequence 2, Appl1

ALIGNMENTS

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RESULT 1
US-09-398-412B-13
; Sequence 13, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related r
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398, 412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-398-412B-13

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Best Local Similarity 100.0%; Pred. No. 2.9e-96;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MMTLSGALCFRMDKSAKVLTLHNNQLLAGLHAERVYKGEISVVPNRALDASLSPVIL 60

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QY      121 FLCTSPADQPVRLTQIPEDPAMDAPITDFFPOCD 156
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RESULT 2
US-09-775-046-11
; Sequence 11, Application US/09775046
; Patent No. 6843987
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastlein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775, 046
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; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent version 3.1
; SEQ ID NO 11
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-775-046-11

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Query Match      98.8%; Score 809; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 5,3e-95;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||
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    |||
DB 61 VGGSSQCLSCGTEKPIKLEPVNIMELYGAKESKFTFYRRDMGLTSSPESAAYPGMF 120
    |||
QY 123 CTSPEADQPVRLTQIPEDPAMDAPIIDFYFOOCD 156
    |||
DB 121 CTSPEADQPVRLTQIPEDPAMDAPIIDFYFOOCD 154
    |||

```

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RESULT 3
US-09-417-455-5
; Sequence 5, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-417-455-5

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Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 2 VLSGALCFRMDKSAKLVLYHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVILG 61
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DB 1 VLSGALCFRMDKSAKLVLYHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVILG 60
    |||
QY 62 VGGSSQCLSCGTEKPIKLEPVNIMELYGAKESKFTFYRRDMGLTSSPESAAYPGMF 121
    |||
DB 61 VGGSSQCLSCGTEKPIKLEPVNIMELYGAKESKFTFYRRDMGLTSSPESAAYPGMF 120
    |||
QY 122 LCTSPEDQPVRLTQIPEDPAMDAPIIDFYFOOCD 156
    |||
DB 121 LCTSPEDQPVRLTQIPEDPAMDAPIIDFYFOOCD 155
    |||

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RESULT 4
US-09-348-942-5
; Sequence 5, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/35801
; CURRENT APPLICATION NUMBER: US/09/348,942
; CURRENT FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-348-942-5

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Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 2 VLSGALCFRMDKSAKLVLYHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVILG 61
    |||
DB 1 VLSGALCFRMDKSAKLVLYHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVILG 60
    |||
QY 62 VGGSSQCLSCGTEKPIKLEPVNIMELYGAKESKFTFYRRDMGLTSSPESAAYPGMF 121
    |||
DB 61 VGGSSQCLSCGTEKPIKLEPVNIMELYGAKESKFTFYRRDMGLTSSPESAAYPGMF 120
    |||
QY 122 LCTSPEDQPVRLTQIPEDPAMDAPIIDFYFOOCD 156
    |||
DB 121 LCTSPEDQPVRLTQIPEDPAMDAPIIDFYFOOCD 155
    |||

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RESULT 5
US-09-316-081-5
; Sequence 5, Application US/09316081
; Patent No. 6339141
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/35659

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; CURRENT APPLICATION NUMBER: US/09/316,081
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-316-081-5
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Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
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QY      2 MVLGALCFRMDKDALKVLVYHNNQLAGLHAERKVGEEISVVPNRALDASISPVILG 61
DB      1 MVLGALCFRMDKDALKVLVYHNNQLAGLHAERKVGEEISVVPNRALDASISPVILG 60
QY      62 VQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFFYRRDGLTSSFESAAYPGWF 121
DB      61 VQGSQCLSCGCGVGPFTLTLEPVNIMELYLGAKESKSTFFYRRDGLTSSFESAAYPGWF 120
QY      122 LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 156
DB      121 LCTVPEADQPVRLTQLPENGGMNAFITDFFYFOQCD 155
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RESULT 6
US-09-578-458-5
; Sequence 5, Application US/09578458
; Patent No. 6365726
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; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice
; APPLICANT: Lin, Hai Shan
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/36479
; CURRENT APPLICATION NUMBER: US/09/578,458
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/522,964
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/316,086
; PRIOR FILING DATE: 1999-03-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-578-458-5
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Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
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QY      2 MVLGALCFRMDKDALKVLVYHNNQLAGLHAERKVGEEISVVPNRALDASISPVILG 61
DB      1 MVLGALCFRMDKDALKVLVYHNNQLAGLHAERKVGEEISVVPNRALDASISPVILG 60
QY      62 VQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFFYRRDGLTSSFESAAYPGWF 121
DB      61 VQGSQCLSCGCGVGPFTLTLEPVNIMELYLGAKESKSTFFYRRDGLTSSFESAAYPGWF 120
QY      122 LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 156
DB      121 LCTVPEADQPVRLTQLPENGGMNAFITDFFYFOQCD 155
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RESULT 7
US-09-522-964A-5
; Sequence 5, Application US/09522964A
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; Patent No. 6372892
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Lin, Hai Shan
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/36210
; CURRENT APPLICATION NUMBER: US/09/522,964A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/316,086
; PRIOR FILING DATE: 1999-03-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-964A-5
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Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
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QY      2 MVLGALCFRMDKDALKVLVYHNNQLAGLHAERKVGEEISVVPNRALDASISPVILG 61
DB      1 MVLGALCFRMDKDALKVLVYHNNQLAGLHAERKVGEEISVVPNRALDASISPVILG 60
QY      62 VQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFFYRRDGLTSSFESAAYPGWF 121
DB      61 VQGSQCLSCGCGVGPFTLTLEPVNIMELYLGAKESKSTFFYRRDGLTSSFESAAYPGWF 120
QY      122 LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 156
DB      121 LCTVPEADQPVRLTQLPENGGMNAFITDFFYFOQCD 155
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RESULT 8
US-09-457-626-5
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; Sequence 5, Application US/09457626
; Patent No. 6426191
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36010
; CURRENT APPLICATION NUMBER: US/09/457,626
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: US 09/417,455
; EARLIER FILING DATE: 1999-10-13
; EARLIER APPLICATION NUMBER: US 09/348,942
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-626-5

Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Oy 2 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRDLASISPVILG 61
Db 1 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRDLASISPVILG 60

Oy 62 VGGSGCSCGTEKGPILKLEPVNIMELYLGAKEKSFYFRDMGLTSSPESAAYPGWF 121
Db 61 VGGSGCSCGCGVGEPTLTLEPVNIMELYLGAKEKSFYFRDMGLTSSPESAAYPGWF 120

Oy 122 LCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
Db 121 LCTVPADQPVRLTQLPENGGMNAPITDFYFOQCD 155

RESULT 9
US-09-576-008-5
; Sequence 5, Application US/09576008
; Patent No. 6541623
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice Suk-Yue
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36456
; CURRENT APPLICATION NUMBER: US/09/576,008
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/523,552
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/457,626
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 09/417,455
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-576-008-5

Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Oy 2 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRDLASISPVILG 61
Db 1 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRDLASISPVILG 60
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```

Db 1 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRDLASISPVILG 60
Oy 62 VGGSGCSCGTEKGPILKLEPVNIMELYLGAKEKSFYFRDMGLTSSPESAAYPGWF 121
Db 61 VGGSGCSCGCGVGEPTLTLEPVNIMELYLGAKEKSFYFRDMGLTSSPESAAYPGWF 120

Oy 122 LCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
Db 121 LCTVPADQPVRLTQLPENGGMNAPITDFYFOQCD 155

RESULT 10
US-09-949-016-6827
; Sequence 6827, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6827
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6827

Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Oy 2 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRDLASISPVILG 61
Db 1 MVLGALCFRMDKSLKLYLHNNQLLAGLHAEKVIKGEISVVPNRDLASISPVILG 60

Oy 62 VGGSGCSCGTEKGPILKLEPVNIMELYLGAKEKSFYFRDMGLTSSPESAAYPGWF 121
Db 61 VGGSGCSCGCGVGEPTLTLEPVNIMELYLGAKEKSFYFRDMGLTSSPESAAYPGWF 120

Oy 122 LCTSPADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
Db 121 LCTVPADQPVRLTQLPENGGMNAPITDFYFOQCD 155

RESULT 11
US-09-775-046-2
; Sequence 2, Application US/09775046
; Patent No. 6843987
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES, RECEPTORS, RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775,046
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 155
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-775-046-2
Query Match      89.6%; Score 734; DB 2; Length 155;
Best Local Similarity 91.0%; Pred. No. 2e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      2  MVLGALCFRMDKSLKLYLHNNQLAGLHAERKVIKGEISVVPNRALDASLSPVILG 61
DB      1  MVLGALCFRMDKSLKLYLHNNQLAGLHAERKVIKGEISVVPNRALDASLSPVILG 60

QY      62  VGGSGGCLSCGVEGEPFLTLLEPVNIMELYLGAKSKSFTFYRDMGLTSSFESAAYPGWF 121
DB      61  VGGSGGCLSCGVEGEPFLTLLEPVNIMELYLGAKSKSFTFYRDMGLTSSFESAAYPGWF 120

QY      122  LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 156
DB      121  LCTVPADQPVRLTQLPENGGMNAPITDFFYFOQCD 155

RESULT 12
US-09-949-016-9356
; Sequence 9356, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYOMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9356
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9356

Query Match      89.6%; Score 734; DB 2; Length 187;
Best Local Similarity 91.0%; Pred. No. 2.7e-85;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      2  MVLGALCFRMDKSLKLYLHNNQLAGLHAERKVIKGEISVVPNRALDASLSPVILG 61
DB      3  MVLGALCFRMDKSLKLYLHNNQLAGLHAERKVIKGEISVVPNRALDASLSPVILG 92

QY      62  VGGSGGCLSCGVEGEPFLTLLEPVNIMELYLGAKSKSFTFYRDMGLTSSFESAAYPGWF 121
DB      93  VGGSGGCLSCGVEGEPFLTLLEPVNIMELYLGAKSKSFTFYRDMGLTSSFESAAYPGWF 152

QY      122  LCTSPADQPVRLTQIPEDPAMDAPITDFFYFOQCD 156
DB      153  LCTVPADQPVRLTQLPENGGMNAPITDFFYFOQCD 187

RESULT 13
US-09-417-455-3
; Sequence 3, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
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; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-417-455-3

Query Match      48.0%; Score 393; DB 2; Length 80;
Best Local Similarity 90.0%; Pred. No. 2.7e-42;
Matches 72; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      77  PINKLEPVNIMELYLGAKSKSFTFYRDMGLTSSFESAAYPGWFLCTSPADQPVRLTQ 136
DB      1  PINKLEPVNIMELYLGAKSKSFTFYRDMGLTSSFESAAYPGWFLCTSPADQPVRLTQ 60

QY      137  IPEDPAMDAPITDFFYFOQCD 156
DB      61  LPENGGMNAPITDFFYFOQCD 80

RESULT 14
US-09-348-942-3
; Sequence 3, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/35801
; CURRENT APPLICATION NUMBER: US/09/348,942
; CURRENT FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 80
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Thu Apr 6 16:26:16 2006

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2006, 15:07:22 ; Search time 45 Seconds
(without alignments)
1448.475 Million cell updates/sec

Title: US-09-770-528-2
Perfect score: 819
Sequence: 1 NMVLSGALCFRKMDSALKVL.....IPEDPAWDAPITDFYQGD 156

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	819	100.0	156	3	US-09-770-528-2
2	819	100.0	156	3	US-09-965-640-2
3	819	100.0	156	4	US-10-267-791-2
4	819	100.0	156	4	US-10-042-865-124
5	819	100.0	156	4	US-10-695-195-13
6	819	100.0	156	4	US-10-694-978-13
7	819	100.0	156	4	US-10-734-985-2
8	819	100.0	156	5	US-10-948-920-2
9	814	99.4	155	4	US-10-042-865-123
10	809	98.8	154	3	US-09-775-046-11
11	768	93.8	146	3	US-09-730-617-55
12	734	89.6	155	3	US-09-730-617-61
13	734	89.6	155	3	US-09-730-617-80
14	734	89.6	155	3	US-09-730-617-96
15	734	89.6	155	3	US-09-775-046-2
16	734	89.6	155	3	US-09-965-640-4
17	734	89.6	155	4	US-10-006-867-152
18	734	89.6	155	4	US-10-003-671A-5
19	734	89.6	155	4	US-10-063-547-152
20	734	89.6	155	4	US-10-063-551-152
21	734	89.6	155	4	US-10-139-833-10
22	734	89.6	155	4	US-10-063-616-152
23	734	89.6	155	4	US-10-063-569-152
24	734	89.6	155	4	US-10-063-513-152
25	734	89.6	155	4	US-10-063-515-152
26	734	89.6	155	4	US-10-063-512-152
27	734	89.6	155	4	US-10-063-502-152

28	734	89.6	155	4	US-10-063-549-152	Sequence 152, App
29	734	89.6	155	4	US-10-063-554-152	Sequence 152, App
30	734	89.6	155	4	US-10-063-553-152	Sequence 152, App
31	734	89.6	155	4	US-10-063-518-152	Sequence 152, App
32	734	89.6	155	4	US-10-063-598-152	Sequence 152, App
33	734	89.6	155	4	US-10-227-693-152	Sequence 152, App
34	734	89.6	155	4	US-10-267-791-5	Sequence 5, Appl1
35	734	89.6	155	4	US-10-063-563-152	Sequence 152, App
36	734	89.6	155	4	US-10-063-555-152	Sequence 152, App
37	734	89.6	155	4	US-10-063-557-152	Sequence 152, App
38	734	89.6	155	4	US-10-063-567-152	Sequence 152, App
39	734	89.6	155	4	US-10-063-538-152	Sequence 152, App
40	734	89.6	155	4	US-10-063-599-152	Sequence 152, App
41	734	89.6	155	4	US-10-063-595-152	Sequence 152, App
42	734	89.6	155	4	US-10-205-821-3	Sequence 3, Appl1
43	734	89.6	155	4	US-10-223-085-316	Sequence 316, App
44	734	89.6	155	4	US-10-223-084-316	Sequence 316, App
45	734	89.6	155	4	US-10-223-086-316	Sequence 316, App

ALIGNMENTS

RESULT 1
US-09-770-528-2
Sequence 2, Application US/09770528
Patent No. US20020164332A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Sana, Theodore R.
Bazan, Fernando J.
Kastelen, Robert A.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,528
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/130,972
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/055,111
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: US 09/062,866
FILING DATE: 20-APR-1998
APPLICATION NUMBER: US 09/097,976
FILING DATE: 16-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0725K2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-770-528-2

Query Match 100.0%; Score 819; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60

QY 61 GVGGSGCSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGCSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120

QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOCCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOCCD 156

RESULT 2
US-09-965-640-2

Sequence 2, Application US/09965640
Publication No. US20020187122A1
GENERAL INFORMATION:
APPLICANT: Sime, John E.
TITLE OF INVENTION: IL-1 DELTA DNA AND POLYPEPTIDES
FILE REFERENCE: 0315-C
CURRENT APPLICATION NUMBER: US/09/965,640
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/612,921
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 156
TYPE: PRT
ORGANISM: Mus musculus
US-09-965-640-2

Query Match 100.0%; Score 819; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60

QY 61 GVGGSGCSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGCSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120

QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOCCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOCCD 156

RESULT 3

US-10-267-791-2
Sequence 2, Application US/10267791
Publication No. US20030059892A1
GENERAL INFORMATION:

APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF THE TANGO-93-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334-200001 (formerly 09404/086001)
CURRENT APPLICATION NUMBER: US/10/267,791
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/369,693
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: US 09/131,263
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 156
TYPE: PRT
ORGANISM: Mus musculus
US-10-267-791-2

Query Match 100.0%; Score 819; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGEISVVPNRALDASLSPVIL 60

QY 61 GVGGSGCSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGCSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120

QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOCCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOCCD 156

RESULT 4
US-10-042-865-124

Sequence 124, Application US/10042865
Publication No. US20040029216A1
GENERAL INFORMATION:

APPLICANT: Padigaru, Muralidhara
APPLICANT: Li, Li
APPLICANT: Zernhusen, Bryan D
APPLICANT: Casman, Stacie J
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly
APPLICANT: Zhong, Mei
APPLICANT: Gangoli, Esba A
APPLICANT: Burgess, Catherine E
APPLICANT: Patlurajan, Meera
APPLICANT: Vernet, Corine A.M
APPLICANT: Taylor, Sarah
APPLICANT: Tchernev, Velizar T
APPLICANT: Miller, Charles E
APPLICANT: Guo, Xiaojia
APPLICANT: Boldog, Ference L
APPLICANT: Grosse, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Gerlach, Valerie L
APPLICANT: Beiniger, Shlomit R
APPLICANT: Rothenberg, Mark E
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Malvankar, Uriel M
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John
APPLICANT: Smitson, Gienna
APPLICANT: Gunther, Erik
APPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: US/10/042,865
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/272,338
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR FILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 264
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 124
LENGTH: 156
TYPE: PRT
ORGANISM: Mus musculus
US-10-042-865-124

Query Match 100.0%; Score 819; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2,2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRKMDSALKVLYLHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRKMDSALKVLYLHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 5

US-10-695-195-13
Sequence 13, Application US/10695195
Publication No. US20040068099A1

GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: DMAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/695,195
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-695-195-13

Query Match 100.0%; Score 819; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2,2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRKMDSALKVLYLHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRKMDSALKVLYLHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 6

US-10-694-978-13
Sequence 13, Application US/10694978
Publication No. US20040087766A1

GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: DMAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/694,978
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-694-978-13

Query Match 100.0%; Score 819; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2,2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRKMDSALKVLYLHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRKMDSALKVLYLHNNQLLAGGLHAEKVIKGEISVVPNRALDASISPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 7

US-10-734-985-2
; Sequence 2, Application US/10734985
; Publication No. US20040142420A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TANGO-93-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-369001
; CURRENT APPLICATION NUMBER: US/10/734,985
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US/10/134,410
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 09/131,263
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: US 09/369,693
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-734-985-2

Query Match 100.0%; Score 819; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2,2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTLSGALCFRMDASALKVLYLHNNQLAGLHAERKIKGEEISVVPNRALDASLSPVIL 60
DB 1 MMTLSGALCFRMDASALKVLYLHNNQLAGLHAERKIKGEEISVVPNRALDASLSPVIL 60
QY 61 GVGGSGQLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOOCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOOCD 156
RESULT 8
US-10-948-920-2
; Sequence 2, Application US/10948920
; Publication No. US20050058625A1
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; TITLE OF INVENTION: IL-1 DELTA DNA AND POLYPEPTIDES
; FILE REFERENCE: 0315-C
; CURRENT APPLICATION NUMBER: US/10/948,920
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US/09/965,640
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/612,921
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-948-920-2

Query Match 100.0%; Score 819; DB 5; Length 156;
Best Local Similarity 100.0%; Pred. No. 2,2e-84;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTLSGALCFRMDASALKVLYLHNNQLAGLHAERKIKGEEISVVPNRALDASLSPVIL 60
DB 1 MMTLSGALCFRMDASALKVLYLHNNQLAGLHAERKIKGEEISVVPNRALDASLSPVIL 60

QY 61 GVGGSGQLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
DB 61 GVGGSGQLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOOCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOOCD 156

RESULT 9

US-10-042-865-123
; Sequence 123, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangoli, Bsha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Paturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchertnev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Reference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-042-865-123

Query Match 99.4%; Score 814; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. 8,1e-84;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MMTLSGALCFRMDASALKVLYLHNNQLAGLHAERKIKGEEISVVPNRALDASLSPVIL 61
DB 1 MMTLSGALCFRMDASALKVLYLHNNQLAGLHAERKIKGEEISVVPNRALDASLSPVIL 60

QY 62 VGGSGQCLSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 121
DB 61 VGGSGQCLSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 120
QY 122 LCTSPBADQVRLTQIPEDPAMDAPITDIFYPOCCD 156
DB 121 LCTSPBADQVRLTQIPEDPAMDAPITDIFYPOCCD 155

RESULT 10
US-09-775-046-11
; Sequence 11, Application US/09775046
; Patent No. US20020102234A1
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-775-046-11

Query Match 98.8%; Score 809; DB 3; Length 154;
Best Local Similarity 100.0%; Pred. No. 3e-83;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSGALCFRMDKSAKLYLHNNQLLAGLHAERKVIKGEISVVPNRALDASLSPVILGV 62
DB 1 VLSGALCFRMDKSAKLYLHNNQLLAGLHAERKVIKGEISVVPNRALDASLSPVILGV 60
QY 63 QGSGQCLSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 122
DB 61 QGSGQCLSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 120
QY 123 CTSPEADQVRLTQIPEDPAMDAPITDIFYPOCCD 156
DB 121 CTSPEADQVRLTQIPEDPAMDAPITDIFYPOCCD 154

RESULT 11
US-09-730-617-55
; Sequence 55, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shinkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zeehuysen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-617-55

Query Match 93.8%; Score 768; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.2e-78;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CFRMKDSALKVLYLHNNQLLAGLHAERKVIKGEISVVPNRALDASLSPVILGVGGSGQC 68
DB 1 CFRMKDSALKVLYLHNNQLLAGLHAERKVIKGEISVVPNRALDASLSPVILGVGGSGQC 60
QY 69 LSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWFLCTSPBA 128
DB 61 LSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWFLCTSPBA 120
QY 129 DQVRLTQIPEDPAMDAPITDIFYPOCCD 154
DB 121 DQVRLTQIPEDPAMDAPITDIFYPOCCD 146

RESULT 12
US-09-730-617-61
; Sequence 61, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shinkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zeehuysen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-617-61

Query Match 89.6%; Score 734; DB 3; Length 155;
Best Local Similarity 91.0%; Pred. No. 9.6e-75;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 MUISGALCFRMDKSAKLYLHNNQLLAGLHAERKVIKGEISVVPNRALDASLSPVILGV 61
DB 1 MUISGALCFRMDKSAKLYLHNNQLLAGLHAERKVIKGEISVVPNRALDASLSPVILGV 60
QY 62 VGGSGQCLSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 121
DB 61 VGGSGQCLSCGTEKGPILKLEPNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 120
QY 122 LCTSPBADQVRLTQIPEDPAMDAPITDIFYPOCCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

RESULT 13
US-09-730-617-80

Sequence 80, Application US/09730617
Patent No. US20020068279A1

GENERAL INFORMATION:

APPLICANT: Burgess, Catherine E

APPLICANT: Prayaga, Sudhirdas K

APPLICANT: Shinkels, Richard A

APPLICANT: Raestelli, Luca

APPLICANT: Zernhusen, Bryan D

APPLICANT: Mezes, Peter S

TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam

FILE REFERENCE: 15966-609

CURRENT APPLICATION NUMBER: US/09/730,617

CURRENT FILING DATE: 2000-12-05

PRIOR APPLICATION NUMBER: 60/169,056

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 60/169,886

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 60/169,866

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 60/170,252

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: 60/175,740

PRIOR FILING DATE: 2000-01-12

NUMBER OF SEQ ID NOS: 100

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 80

LENGTH: 155

TYPE: PRT

ORGANISM: Homo sapiens

US-09-730-617-80

Query Match

Best Local Similarity 91.0%; Pred. No. 9.6e-75;

Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 MVLGALCFPMKDSALKVLYLHNNQLLAGLHAEKVIKGEISVPPRALDASISPVILG 61

Db 1 MVLGALCFPMKDSALKVLYLHNNQLLAGLHAEKVIKGEISVPPRALDASISPVILG 60

QY 62 VGGSGQLSCGTEKGPITLKEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWF 121

Db 61 VGGSGQLSCGTEKGPITLKEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWF 120

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

PRIOR APPLICATION NUMBER: 60/169,866

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 60/170,252

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: 60/175,740

PRIOR FILING DATE: 2000-01-12

NUMBER OF SEQ ID NOS: 100

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 96

LENGTH: 155

TYPE: PRT

ORGANISM: Homo sapiens

US-09-730-617-96

Query Match

Best Local Similarity 91.0%; Pred. No. 9.6e-75;

Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 2 MVLGALCFPMKDSALKVLYLHNNQLLAGLHAEKVIKGEISVPPRALDASISPVILG 61

Db 1 MVLGALCFPMKDSALKVLYLHNNQLLAGLHAEKVIKGEISVPPRALDASISPVILG 60

QY 62 VGGSGQLSCGTEKGPITLKEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWF 121

Db 61 VGGSGQLSCGTEKGPITLKEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWF 120

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

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QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

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QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Db 121 LCTVPEADQPVRLTQLPENGMNAPITDFYFOQCD 155

QY 122 LCTSPBADQPVRLTQLPENGMNAPITDFYFOQCD 156

Search completed: April 5, 2006, 15:08:15

Job time : 46 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2006, 15:08:22 ; Search time 14 Seconds

(without alignments)
347.568 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 819
Sequence: 1 MMTLSGALCFRMDKSLKVL.....IPEDPAMDAPITDPTFOCD 156

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB pep.*
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5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB pep.*
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8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	734	89.6	155	6	US-10-063-703-152 Sequence 152, App
2	734	89.6	155	7	US-11-102-240-152 Sequence 152, App
3	734	89.6	155	7	US-11-103-195-152 Sequence 152, App
4	307.5	37.5	143	6	US-10-995-561-568 Sequence 568, App
5	307.5	37.5	143	6	US-10-995-561-569 Sequence 569, App
6	307.5	37.5	143	6	US-10-995-561-570 Sequence 570, App
7	307.5	37.5	152	7	US-11-097-993-3 Sequence 3, Appl
8	307.5	37.5	152	7	US-11-097-993-3 Sequence 3, Appl
9	307.5	37.5	153	7	US-11-097-993-5 Sequence 5, Appl
10	307.5	37.5	153	7	US-11-097-993-5 Sequence 5, Appl
11	307.5	37.5	153	7	US-11-175-734-5 Sequence 5, Appl
12	307.5	37.5	159	6	US-10-995-561-567 Sequence 567, App
13	307.5	37.5	159	7	US-11-097-993-6 Sequence 6, Appl
14	307.5	37.5	159	7	US-11-097-993-6 Sequence 6, Appl
15	307.5	37.5	177	6	US-10-995-561-571 Sequence 571, App
16	307.5	37.5	177	6	US-10-876-787-4 Sequence 4, Appl
17	307.5	37.5	177	7	US-11-097-993-2 Sequence 2, Appl
18	307.5	37.5	177	7	US-11-097-993-2 Sequence 2, Appl
19	306.5	37.4	153	6	US-10-063-703-142 Sequence 12, App
20	191.5	23.4	193	7	US-11-102-240-142 Sequence 142, App
21	191.5	23.4	193	7	US-11-103-195-142 Sequence 142, App
22	191.5	23.4	193	7	US-11-103-195-142 Sequence 142, App
23	122	14.9	269	6	US-10-995-561-535 Sequence 534, App
24	122	14.9	303	6	US-10-995-561-534 Sequence 534, App
25	113	13.8	33	7	US-11-072-170A-16 Sequence 16, Appl

26	84	10.3	1433	7	US-11-094-519A-40 Sequence 40, Appl
27	81	9.9	715	7	US-11-087-099-2922 Sequence 2922, Ap
28	72.5	8.9	237	7	US-11-096-568A-21493 Sequence 21493, A
29	72.5	8.9	247	7	US-11-096-568A-21492 Sequence 21492, A
30	72.5	8.9	256	7	US-11-096-568A-21491 Sequence 21491, A
31	72	8.8	666	7	US-11-096-568A-14747 Sequence 14747, A
32	72	8.8	761	7	US-11-096-568A-14746 Sequence 14746, A
33	72	8.8	911	7	US-11-096-568A-14745 Sequence 14745, A
34	71.5	8.7	4060	6	US-10-922-232B-55 Sequence 55, Appl
35	71.5	8.7	6738	7	US-10-922-232B-55 Sequence 55, Appl
36	70.5	8.6	6738	7	US-11-096-568A-26923 Sequence 26923, A
37	70.5	8.6	699	7	US-11-096-568A-26922 Sequence 26922, A
38	70.5	8.6	699	7	US-10-770-726-88 Sequence 88, Appl
39	70.5	8.6	857	7	US-11-090-617-686 Sequence 686, App
40	70.5	8.5	29	7	US-11-072-170A-17 Sequence 17, Appl
41	69.5	8.5	311	7	US-11-096-568A-28854 Sequence 28854, A
42	69.5	8.5	340	7	US-11-096-568A-27013 Sequence 27013, A
43	69.5	8.5	340	7	US-11-096-568A-27013 Sequence 27013, A
44	69.5	8.5	366	7	US-11-096-568A-28853 Sequence 28853, A
45	69.5	8.5	366	7	US-11-096-568A-28853 Sequence 28853, A

ALIGNMENTS

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RESULT 1
US-10-063-703-152
; Sequence 152, Application US/10063703
; Publication No. US20060008901A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlt, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,703
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 152
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-703-152

Query Match      89.6%; Score 734; DB 6; Length 155;
Best Local Similarity 91.0%; Pred No. 1,1e-72;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      2 MVLGALCFRMDKSLKVLTHNNQLAGLAEKVIKKEBSVVRNALDASLPYILG 61
DB      1 MMTLSGALCFRMDKSLKVLTHNNQLAGLAEKVIKKEBSVVRNALDASLPYILG 60

QY      62 VGGSGCSCSGEKEPILKLEPVNIMELYLKAKESKSFYPRDKLTSFESAAYPGW 121
DB      61 VGGSGCSCSGVGEETLTLEFPVNIMELYLKAKESKSFYPRDKLTSFESAAYPGW 120

QY      122 LCTSPADQPVRLTQIPEDPAMDAPITDPTFOCD 156
DB      121 LCTVPEADQPVRLTQIPEDPAMDAPITDPTFOCD 155

RESULT 2
US-11-102-240-152
; Sequence 152, Application US/11102240
; Publication No. US20050260647A1

```

```
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
TITLE OF INVENTION: ESOPHAGEAL TUMOR
FILE REFERENCE: P3230C1306C
CURRENT APPLICATION NUMBER: US/11/102,240
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 10/063662
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 199-12-09
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 152
LENGTH: 155
TYPE: PRT
ORGANISM: Homo Sapien
US-11-102-240-152

Query Match      89.6%; Score 734; DB 7; Length 155;
Best Local Similarity 91.0%; Pred. No. 1,1e-72;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      2 MVLGALCFRMKDSALKVLYLHNNQLLAGLHAKEVYKKEEISVVENRALDASLPVILG 61
DB      1 MVLGALCFRMKDSALKVLYLHNNQLLAGLHAGKVIKKEEISVVENRMWDASLPVILG 60
QY      62 VOGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGWF 121
DB      61 VOGSGQCLSCGVQGEPTLTLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGWF 120

QY      122 LCTSPADQPVRLTOIPEDPAMDAPITDFYFOOCD 156
DB      121 LCTVPEADQPVRLTOIPENGGMNAPITDFYFOOCD 155

RESULT 3
US-11-103-195-152
Sequence 152, Application US/11103195
Publication No. US20060051779A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230C166C1
CURRENT APPLICATION NUMBER: US/11/103,195
CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: 10/063743
PRIOR FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 152
LENGTH: 155
TYPE: PRT
ORGANISM: Homo Sapien
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US-11-103-195-152

Query Match      89.6%; Score 734; DB 7; Length 155;
Best Local Similarity 91.0%; Pred. No. 1,1e-72;
Matches 141; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      2 MVLGALCFRMKDSALKVLYLHNNQLLAGLHAKEVYKKEEISVVENRALDASLPVILG 61
DB      1 MVLGALCFRMKDSALKVLYLHNNQLLAGLHAGKVIKKEEISVVENRMWDASLPVILG 60
QY      62 VOGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGWF 121
DB      61 VOGSGQCLSCGVQGEPTLTLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGWF 120

QY      122 LCTSPADQPVRLTOIPEDPAMDAPITDFYFOOCD 156
DB      121 LCTVPEADQPVRLTOIPENGGMNAPITDFYFOOCD 155

RESULT 4
US-10-995-561-568
Sequence 568, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 568
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-568

Query Match      37.5%; Score 307.5; DB 6; Length 143;
Best Local Similarity 48.0%; Pred. No. 3,1e-26;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY      10 FRMKDSALKVLYLHNNQLLAGLHAKEVYKKEEISVVENRALDASLP--VILGVOGSGQ 67
DB      4 FRIMDVNOKTFYLRNNQLVAGYLGQPNVNLBEKIDVP-----IEPRALFLGHHGKA 56
QY      68 CLSC--GTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGWFILCT 124
DB      57 CLSCVSGDETR--IQLEAVNITDISENRKQDRFAFIRSDSQPTTSFESAACPGWFILCT 114

QY      125 SPADQPVRLTOIPEDPAMDAPITDFYFOO 154
DB      115 AMEADQPVSLTNMPD---GVMTKTFYFOE 141

RESULT 5
US-10-995-561-569
Sequence 569, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 569
LENGTH: 143
TYPE: PRT
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```

; ORGANISM: Homo sapiens
US-10-995-561-569

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 6; Length 143;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

Qy 10 FRMDSALKVLYLHNNQLAGLHAKEYIKGEISVVPNRALDASLSP--VILGVQGSQ 67
Db 4 FRIMDVNQKTFYLRNNQLVAGYLOGPNNLEKIDVP-----IEPHALFLGIHGKM 56

Qy 68 CLSC---GTEKGPILKLEPNVIMELYGAKESKSTFYRRDMGLTSSFESAAYPGWFLCT 124
Db 57 CLSCVKSDETR--LQLEAVNITDLSNRKQDKRFAFRSDSGPTTSFESAACPGWFLCT 114

Qy 125 SPBADOVRLTQIPEDPAMDAPITDPYFQO 154
Db 115 AMEADQPVSLTNMPDE---GVMVTKFYFOE 141

RESULT 6
US-10-995-561-570
; Sequence 570, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 570
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-570

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 6; Length 143;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

Qy 10 FRMDSALKVLYLHNNQLAGLHAKEYIKGEISVVPNRALDASLSP--VILGVQGSQ 67
Db 4 FRIMDVNQKTFYLRNNQLVAGYLOGPNNLEKIDVP-----IEPHALFLGIHGKM 56

Qy 68 CLSC---GTEKGPILKLEPNVIMELYGAKESKSTFYRRDMGLTSSFESAAYPGWFLCT 124
Db 57 CLSCVKSDETR--LQLEAVNITDLSNRKQDKRFAFRSDSGPTTSFESAACPGWFLCT 114

Qy 125 SPBADOVRLTQIPEDPAMDAPITDPYFQO 154
Db 115 AMEADQPVSLTNMPDE---GVMVTKFYFOE 141

RESULT 7
US-11-097-993-3
; Sequence 3, Application US/11097993
; Publication No. US20050271618A1
; GENERAL INFORMATION:
; APPLICANT: Kerdin, Bruce
; TITLE OF INVENTION: METHODS OF REDUCING AGGREGATION OF IL-1RA
; FILE REFERENCE: 06843.0093-00000
; CURRENT APPLICATION NUMBER: US/11/097,993
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/558,879
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/559,161
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/601,216
```

```

; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/601,229
; PRIOR FILING DATE: 2004-08-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-097-993-3

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 7; Length 152;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

Qy 10 FRMDSALKVLYLHNNQLAGLHAKEYIKGEISVVPNRALDASLSP--VILGVQGSQ 67
Db 13 FRIMDVNQKTFYLRNNQLVAGYLOGPNNLEKIDVP-----IEPHALFLGIHGKM 65

Qy 68 CLSC---GTEKGPILKLEPNVIMELYGAKESKSTFYRRDMGLTSSFESAAYPGWFLCT 124
Db 66 CLSCVKSDETR--LQLEAVNITDLSNRKQDKRFAFRSDSGPTTSFESAACPGWFLCT 123

Qy 125 SPBADOVRLTQIPEDPAMDAPITDPYFQO 154
Db 124 AMEADQPVSLTNMPDE---GVMVTKFYFOE 150

RESULT 8
US-11-097-453-3
; Sequence 3, Application US/11097453
; Publication No. US20050282752A1
; GENERAL INFORMATION:
; APPLICANT: Kerdin, Bruce
; TITLE OF INVENTION: IL-1RA VARIANTS
; FILE REFERENCE: 06843.0092-00000
; CURRENT APPLICATION NUMBER: US/11/097,453
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/558,879
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 60/601,216
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/559,161
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-097-453-3

Query Match
Best Local Similarity 37.5%; Score 307.5; DB 7; Length 152;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

Qy 10 FRMDSALKVLYLHNNQLAGLHAKEYIKGEISVVPNRALDASLSP--VILGVQGSQ 67
Db 13 FRIMDVNQKTFYLRNNQLVAGYLOGPNNLEKIDVP-----IEPHALFLGIHGKM 65

Qy 68 CLSC---GTEKGPILKLEPNVIMELYGAKESKSTFYRRDMGLTSSFESAAYPGWFLCT 124
Db 66 CLSCVKSDETR--LQLEAVNITDLSNRKQDKRFAFRSDSGPTTSFESAACPGWFLCT 123

Qy 125 SPBADOVRLTQIPEDPAMDAPITDPYFQO 154
Db 124 AMEADQPVSLTNMPDE---GVMVTKFYFOE 150

RESULT 9
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```
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-567

Query Match
  37.5%; Score 307.5; DB 6; Length 159;
  48.0%; Pred. No. 3.6e-26;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMDSALKVLYLHNNOLLAGLHAKEYIKGEISVVPNRALDASLP--VILGVQGSQ 67
DB 20 FRIMVNOKTFYLRNNQVAGYLQGPVNLBEKIDVP-----IEPHALFLGIHGKM 72
QY 68 CLSC---GTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGMFLCT 124
DB 73 CLSCVKSGBETR--LQLEAVNITDLSNRKODKRFARIRSDSGPTTSFESAACPGMFLCT 130
QY 125 SPBADOVRLTQIPEDPAMDAPITDFFYFQ 154
DB 131 AMEADQPVSLTNMPDE---GVMVTKFYFQ 157

RESULT 13
US-11-097-993-6
Sequence 6, Application US/11097993
Publication No. US20050271618A1
GENERAL INFORMATION:
APPLICANT: Raibekas, Andrei
TITLE OF INVENTION: METHODS OF REDUCING AGGREGATION OF IL-1RA
FILE REFERENCE: 06843.0093-00000
CURRENT APPLICATION NUMBER: US/11/097,993
PRIOR FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: 60/558,879
PRIOR FILING DATE: 2004-04-02
PRIOR APPLICATION NUMBER: 60/559,161
PRIOR FILING DATE: 2004-04-02
PRIOR APPLICATION NUMBER: 60/601,216
PRIOR FILING DATE: 2004-08-12
PRIOR APPLICATION NUMBER: 60/601,229
PRIOR FILING DATE: 2004-08-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6
LENGTH: 159
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: icIL-1ra sequence
US-11-097-993-6

Query Match
  37.5%; Score 307.5; DB 7; Length 159;
  48.0%; Pred. No. 3.6e-26;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMDSALKVLYLHNNOLLAGLHAKEYIKGEISVVPNRALDASLP--VILGVQGSQ 67
DB 20 FRIMVNOKTFYLRNNQVAGYLQGPVNLBEKIDVP-----IEPHALFLGIHGKM 72
QY 68 CLSC---GTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGMFLCT 124
DB 73 CLSCVKSGBETR--LQLEAVNITDLSNRKODKRFARIRSDSGPTTSFESAACPGMFLCT 130
QY 125 SPBADOVRLTQIPEDPAMDAPITDFFYFQ 154
DB 131 AMEADQPVSLTNMPDE---GVMVTKFYFQ 157

RESULT 14
US-11-097-453-13
Sequence 13, Application US/11097453
Publication No. US20050282752A1
GENERAL INFORMATION:
APPLICANT: Raibekas, Andrei
```

```
APPLICANT: Kevin, Bruce
TITLE OF INVENTION: IL-1RA VARIANTS
FILE REFERENCE: 06843.0092-00000
CURRENT APPLICATION NUMBER: US/11/097,453
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: 60/558,879
PRIOR FILING DATE: 2004-04-02
PRIOR APPLICATION NUMBER: 60/601,216
PRIOR FILING DATE: 2004-08-12
PRIOR APPLICATION NUMBER: 60/601,229
PRIOR FILING DATE: 2004-08-12
PRIOR APPLICATION NUMBER: 60/559,161
PRIOR FILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.3
SEQ ID NO 13
LENGTH: 159
TYPE: PRT
ORGANISM: Homo sapiens
US-11-097-453-13

Query Match
  37.5%; Score 307.5; DB 7; Length 159;
  48.0%; Pred. No. 3.6e-26;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMDSALKVLYLHNNOLLAGLHAKEYIKGEISVVPNRALDASLP--VILGVQGSQ 67
DB 20 FRIMVNOKTFYLRNNQVAGYLQGPVNLBEKIDVP-----IEPHALFLGIHGKM 72
QY 68 CLSC---GTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGMFLCT 124
DB 73 CLSCVKSGBETR--LQLEAVNITDLSNRKODKRFARIRSDSGPTTSFESAACPGMFLCT 130
QY 125 SPBADOVRLTQIPEDPAMDAPITDFFYFQ 154
DB 131 AMEADQPVSLTNMPDE---GVMVTKFYFQ 157

RESULT 15
US-10-995-561-571
Sequence 571, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 571
LENGTH: 177
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-571

Query Match
  37.5%; Score 307.5; DB 6; Length 177;
  48.0%; Pred. No. 4.1e-26;
Matches 72; Conservative 16; Mismatches 45; Indels 17; Gaps 5;

QY 10 FRMDSALKVLYLHNNOLLAGLHAKEYIKGEISVVPNRALDASLP--VILGVQGSQ 67
DB 38 FRIMVNOKTFYLRNNQVAGYLQGPVNLBEKIDVP-----IEPHALFLGIHGKM 90
QY 68 CLSC---GTEKGPILKLEPVNIMELYGAKESKSFYFRDMGLTSSFESAAYPGMFLCT 124
DB 91 CLSCVKSGBETR--LQLEAVNITDLSNRKODKRFARIRSDSGPTTSFESAACPGMFLCT 148
QY 125 SPBADOVRLTQIPEDPAMDAPITDFFYFQ 154
DB 149 AMEADQPVSLTNMPDE---GVMVTKFYFQ 175
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Thu Apr 6 16:26:16 2006

us-09-770-528-2.rapbn

Page 6

Search completed: April 5, 2006, 15:08:44
Job time : 14 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:06:52; Search time 81 Seconds
(without alignments)
846.211 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 156
Sequence: 1 MNTVSGALCFMKDALKVL.....IPEDPAMDAPITDTPFOCCD 156

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 8

Total number of hits satisfying chosen parameters: 596

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

A_Geneseq_21: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *
9: Geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156	100.0	156	2	AAW86284 Rodent in
2	156	100.0	156	2	AAW86284 Rodent in
3	156	100.0	156	2	AAW86284 Rodent in
4	156	100.0	156	2	AAW86284 Rodent in
5	156	100.0	156	2	AAW86284 Rodent in
6	156	100.0	156	2	AAW86284 Rodent in
7	156	100.0	156	2	AAW86284 Rodent in
8	156	100.0	156	2	AAW86284 Rodent in
9	155	99.4	155	4	AAW86672 Murine IL
10	155	99.4	155	4	AAW86672 Murine IL
11	155	99.4	155	4	AAW86672 Murine IL
12	155	99.4	155	4	AAW86672 Murine IL
13	154	98.7	154	4	AAW86672 Murine IL
14	154	98.7	154	4	AAW86672 Murine IL
15	154	98.7	154	4	AAW86672 Murine IL
16	154	98.7	154	4	AAW86672 Murine IL
17	154	98.7	154	4	AAW86672 Murine IL
18	154	98.7	154	4	AAW86672 Murine IL
19	154	98.7	154	4	AAW86672 Murine IL
20	154	98.7	154	4	AAW86672 Murine IL
21	154	98.7	154	4	AAW86672 Murine IL
22	154	98.7	154	4	AAW86672 Murine IL
23	154	98.7	154	4	AAW86672 Murine IL
24	154	98.7	154	4	AAW86672 Murine IL

25	44	28.2	147	5	ABP52030	ABP52030 NOVINTRA
26	44	28.2	147	6	ABP97771	ABP97771 Amino aci
27	44	28.2	147	7	ADCT1444	ADCT1444 Human NOV
28	44	28.2	147	8	ADN33855	ADN33855 Human NOV
29	44	28.2	154	4	AAW86263	AAW86263 Interleuk
30	44	28.2	155	2	AAW86408	AAW86408 Human int
31	44	28.2	155	3	AAW92257	AAW92257 Human int
32	44	28.2	155	3	AAW92256	AAW92256 Human IL-
33	44	28.2	155	3	AAW45062	AAW45062 Human TAN
34	44	28.2	155	3	AAW96936	AAW96936 Human IL-
35	44	28.2	155	4	AAW06655	AAW06655 Human int
36	44	28.2	155	4	AAW86664	AAW86664 Protein e
37	44	28.2	155	4	AAW87601	AAW87601 Human PRO
38	44	28.2	155	4	AAW35262	AAW35262 Interleuk
39	44	28.2	155	4	AAW35260	AAW35260 Human IL-
40	44	28.2	155	5	ABG95926	ABG95926 Human sec
41	44	28.2	155	5	ABW84974	ABW84974 Human PRO
42	44	28.2	155	5	ABW95580	ABW95580 Human ang
43	44	28.2	155	5	ABP52018	ABP52018 NOVINTRA
44	44	28.2	155	5	ABP52034	ABP52034 NOVINTRA
45	44	28.2	155	5	ABP52047	ABP52047 NOVINTRA

ALIGNMENTS

RESULT 1	AAW86284	standard; protein; 156 AA.
ID	AAW86284	
XX	AAW86284	
AC	AAW86284	
DT	19-FEB-1999	(first entry)
XX		
DE	Rodent interleukin (IL)-1 delta polypeptide.	
XX		
KW	Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;	
KW	Inflammatory response; immune system; diagnosis; agonist; antagonist;	
XX	chemokine.	
OS	Mus sp.	
XX		
PN	W09847921-A1.	
XX		
PD	29-OCT-1998.	
XX		
PF	17-APR-1998;	98WO-US006879.
XX		
PR	21-APR-1997;	97US-00837627.
PR	06-AUG-1997;	97US-0055111P.
XX		
PA	(SCHE) SCHERING CORP.	
PI	Hedrick JA, Sana TR, Bazan JF, Kastelein RA;	
XX	WPI, 1998-609976/51.	
DR	N-PSDB; AAV71958.	
XX		
PT	Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g. regulating	
PT	the immune system and inflammatory responses.	
XX		
PS	Claim 1; Page 89-90; 113pp; English.	
XX		
CC	This represents a rodent interleukin (IL)-1 delta polypeptide. The	
CC	invention relates to a recombinant polypeptide that specifically binds	
CC	polyclonal antibodies (Abs) generated against a 12 consecutive amino acid	
CC	segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these	
CC	IL polypeptides are used to regulate a cell involved in an inflammatory	
CC	response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are	
CC	used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and	
CC	the corresponding nucleic acids regulate development and/or the immune	
CC	system, and can be used to diagnose and treat conditions associated with	
CC	abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1	

CC epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
 CC IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
 CC epsilon polypeptides may be used as a soluble polypeptide or as a fusion
 CC protein with another cytokine or chemokine

XX SQ Sequence 156 AA;

Query Match 100.0%; Score 156; DB 2; Length 156;
 Beat Local Similarity 100.0%; Pred. No. 4.2e-159;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGBEISVPPNADASISPVIL 60
 DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGBEISVPPNADASISPVIL 60
 QY 61 GVGGSGQCLSGCTEKGPILKLEPVNIMELYGAKESKSTFYRRDMGLTSSFESAAYPGW 120
 DB 61 GVGGSGQCLSGCTEKGPILKLEPVNIMELYGAKESKSTFYRRDMGLTSSFESAAYPGW 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 2

AA928407 standard; protein; 156 AA.

XX AA928407;

XX 28-SEP-1999 (first entry)

XX Mouse interleukin 1 delta.

XX Interleukin 1 delta; IL-1 delta; glaucoma; ectodermal dysplasia;

XX insulin-dependent diabetes mellitus; wrinkly skin syndrome;

XX T-cell leukemia; lymphoma; tibial muscular dystrophy.

XX Mus musculus.

XX MO9935268-A1.

XX 15-JUL-1999.

XX 08-JAN-1999; 99MO-US000514.

XX 09-JAN-1998; 98US-0071074P.

XX 01-JUN-1998; 98US-0087393P.

XX (IMMV) IMMUNEX CORP.

XX Sims JE;

XX WPI; 1999-458310/38.

XX N-PSDB; AAX89431.

XX Murine and Human interleukin 1 delta DNA, polypeptides and its fragments,
 XX useful as molecular weight markers.

XX Claim 1; Page 67; 72pp; English.

XX The present sequence represents mouse interleukin 1 delta (IL-1 delta).
 CC IL-1 delta proteins are useful for the determination of the molecular
 CC weight of a sample protein. The protein and its fragments are useful as
 CC controls for peptide fragmentation. This is useful for determining the
 CC isoelectric point of a sample protein. Antibodies generated against IL-1
 CC delta and its fragmented peptides can be used to enhance the accuracy of
 CC these molecular weight markers to determine the apparent molecular weight
 CC and isoelectric point of a sample protein. IL-1 delta can be used to
 CC screen for potential inhibitors of activity associated with IL-1 delta
 CC counter-structure molecules. IL-1 delta can also be used as therapeutic
 CC agents for the treatment of diseases mediated by IL-1 delta. IL-1 delta
 CC may be used as a reagent in studying the interleukin 1 (IL-1) signaling

CC pathway, or as a reagent to block IL-1 signaling. The IL-1 delta coding
 CC sequences can be used to identify human chromosome 2, and to identify
 CC genes associated with certain diseases, especially with region 2q11-12,
 CC including glaucoma, ectodermal dysplasia, insulin-dependent diabetes
 CC mellitus, wrinkly skin syndrome, T-cell leukemia/ lymphoma and tibial
 CC muscular dystrophy

XX SQ Sequence 156 AA;

Query Match 100.0%; Score 156; DB 2; Length 156;
 Beat Local Similarity 100.0%; Pred. No. 4.2e-159;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGBEISVPPNADASISPVIL 60
 DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVYKGBEISVPPNADASISPVIL 60
 QY 61 GVGGSGQCLSGCTEKGPILKLEPVNIMELYGAKESKSTFYRRDMGLTSSFESAAYPGW 120
 DB 61 GVGGSGQCLSGCTEKGPILKLEPVNIMELYGAKESKSTFYRRDMGLTSSFESAAYPGW 120
 QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 3

AA92260 standard; protein; 156 AA.

XX AA92260;

XX 10-AUG-2000 (first entry)

XX Murine IL-1 homologue, zllia3.

XX Generic; interleukin-1; IL-1; homologue; zllia3; anti-inflammatory;

XX antagonist; pro-inflammatory; agonist; immunomodulator; antirheumatic;

XX antirheumatic; osteopathic; antibacterial; cytostatic;

XX immunosuppressive; antitumor; antidiabetic; nephrotropic; vasotropic;

XX vulnerable; 2q14.

XX Mus musculus.

XX MO200020595-A1.

XX 13-APR-2000.

XX 08-OCT-1999; 99MO-US023533.

XX 08-OCT-1998; 98US-00169745.

XX (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO, West RR, Clegg CH;

XX WPI; 2000-303780/26.

XX N-PSDB; AAA09198.

XX Proteins useful for treatment of inflammatory conditions such as
 XX rheumatoid arthritis and psoriasis are agonists or antagonists forms of
 XX new interleukin-1 homologue.

XX Example 7; Page 59-60; 64pp; English.

XX This shows an interleukin-1 (IL-1) homologue, designated zllia3. A 350 bp
 CC probe generated from the DNA sequence by PCR using AAA09199-200 was used
 CC to analyze human northern blots. It is believed that zllia3 acts through
 CC IL-1 receptors. In general, zllia3 proteins having a Lys residue at
 CC position 148 will have anti-inflammatory activity (e.g. AA92256), whilst
 CC those having Asp (see AA92254) or Glu at this position will have pro-
 CC inflammatory action. zllia3 is used to modulate an immune response in an
 CC animal (claimed). Antagonists zllia3 forms may be used to treat or

CC prevent chronic inflammatory diseases such as rheumatoid arthritis,
CC osteoarthritis and Lyme arthritis, psoriasis, to reduce tissue damage
CC after ischemia, to treat septic shock, graft-versus-host disease and
CC leukemia. The antagonists may also alleviate inflammatory bowel disease
CC including Crohn's disease and ulcerative colitis, insulin-dependent
CC diabetes mellitus, acute pancreatitis, glomerulonephritis and cerebral
CC ischemia. Agonist forms of zila3 may promote wound healing by IL-1
CC effects on growth factor secretion and cell proliferation. They may also
CC treat infections, especially gastrointestinal infections

CC Sequence 156 AA;

Query Match 100.0%; Score 156; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.2e-159; Indels 0; Gaps 0;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMKDSALKVLYLHNNQLLAGLHAERKVGESIVVPRNALDASLSPYL 60
DB 1 MMVLSGALCFRMKDSALKVLYLHNNQLLAGLHAERKVGESIVVPRNALDASLSPYL 60

QY 61 GVGGSGQLSCGTGKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSFESAAYPGW 120
DB 61 GVGGSGQLSCGTGKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSFESAAYPGW 120

QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDVFYFOCCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDVFYFOCCD 156

RESULT 4
AA45061
ID AA45061 standard; protein, 156 AA.
AC AA45061;
XX
XX 31-MAY-2000 (first entry)
DT
XX
DB Murine TANGO-93 protein.

XX TANGO-93; cytokine; mouse; secreted protein; IL-1 expression; cancer;
XX interleukin-1 receptor antagonist; IL-1ra; inflammation; antiasthmatic;
XX immunosuppressive; antirheumatic; antiarthritic; antipsoriatic; asthma;
XX antiinflammatory; antibacterial; antulcer; cytoskeletal; immunomodulator;
XX osteopathic; dermatological; antidiabetic; psoriasis; ulcerative colitis;
XX graft vs.-host disease; rheumatoid arthritis; inflammatory bowel disease;
XX septic shock; cachexia; Crohn's disease; chronic myelogenous leukaemia;
XX liver disease; diabetes; osteoarthritis; Hodgkin's disease; Lyme disease;
XX autoimmune disease; myasthenia gravis; pharmacogenomic; diagnosis;
XX systemic lupus erythematosus; forensic; transgenic animal.

XX Mus sp.
XX WO200008045-A2.
XX
XX 17-FEB-2000.

XX 06-AUG-1999; 99WO-US017886.
XX
XX 07-AUG-1998; 98US-00131263.

XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
XX Pan Y;
XX
XX WPI; 2000-205669/18.
XX
XX N-PSDB; AA250811.

PT Isolated nucleic acid sequences encoding TANGO-93 polypeptide useful for
PT treating a variety of cellular processes e.g. asthma, rheumatoid
PT arthritis, psoriasis and autoimmune diseases.
XX
XX Claim 9; Fig 1; il3pp; English.

CC The present sequence is the murine TANGO-93, a secreted protein, that
CC belongs to the cytokine superfamily. It plays a role similar to secreted
CC interleukin-1 receptor antagonist (IL-1ra) and its expression is
CC developmentally regulated in liver, heart and bone marrow. TANGO-93
CC modulates immune mediated inflammation and IL-1 gene or protein
CC expression. TANGO-93 is useful as a modulating agent for regulating
CC cellular processes like asthma, graft vs.-host disease, rheumatoid
CC arthritis, psoriasis, inflammatory bowel disease, septic shock,
CC ulcerative colitis, Crohn's disease, chronic myelogenous leukaemia,
CC cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme disease,
CC cachexia, and autoimmune diseases e.g. myasthenia gravis, autoimmune
CC diabetes and systemic lupus erythematosus. Partial TANGO-93 sequences are
CC useful in forensic biology, for diagnostic and prognostic assays,
CC prophylactic and therapeutic treatment and pharmacogenomics. The DNA
CC sequences are useful as hybridisation probes and primers, for isolation
CC of TANGO-93 sequence and for the creation of transgenic animals

CC Sequence 156 AA;

Query Match 100.0%; Score 156; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.2e-159; Indels 0; Gaps 0;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMKDSALKVLYLHNNQLLAGLHAERKVGESIVVPRNALDASLSPYL 60
DB 1 MMVLSGALCFRMKDSALKVLYLHNNQLLAGLHAERKVGESIVVPRNALDASLSPYL 60

QY 61 GVGGSGQLSCGTGKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSFESAAYPGW 120
DB 61 GVGGSGQLSCGTGKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSFESAAYPGW 120

QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDVFYFOCCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDVFYFOCCD 156

RESULT 5
ABU62869
ID ABU62869 standard; protein, 156 AA.
AC ABU62869;
XX
XX 11-SEP-2003 (first entry)
DT
XX
DB Mouse secreted protein TANGO-93.

XX Mouse; TANGO-93; secreted protein; antiasthmatic; immunosuppressive;
XX antirheumatic; antiarthritic; antiinflammatory; antipsoriatic;
XX cytoskeletal; hepatotropic; antidiabetic; dermatological; gene therapy;
XX cytokine superfamily; asthma; graft versus-host disease; cancer;
XX rheumatoid arthritis; psoriasis; inflammatory bowel disease;
XX septic shock; ulcerative colitis; Crohn's disease; liver disease;
XX chronic myelogenous leukaemia; Hodgkin's disease; Lyme's disease;
XX cachexia; autoimmune diabetes; systemic lupus erythematosus.

XX Mus musculus.
XX US2003059892-A1.
XX
XX 27-MAR-2003.

XX 09-OCT-2002; 2002US-00267791.
XX
XX 07-AUG-1998; 98US-00131263.
XX
XX 06-AUG-1999; 99US-00369693.

XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Pan Y;
XX
XX WPI; 2003-521914/49.
XX
XX N-PSDB; ACD26633, ACD26634.

PT New TANGO-93 nucleic acid molecules and polypeptides useful for treating
 PT asthma, graft versus-host disease, rheumatoid arthritis, psoriasis,
 PT inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's
 PT disease, cancer.

PS Claim 8; Fig 1; 43pp; English.

CC The invention describes an isolated nucleic acid molecule (I) designated
 CC as TANGO-93, a secreted protein predicted to be a member of the cytokine
 CC superfamily. The polynucleotides, polypeptides compounds and methods are
 CC useful for treating asthma, graft versus-host disease, rheumatoid
 CC arthritis, psoriasis, inflammatory bowel disease, septic shock,
 CC ulcerative colitis, Crohn's disease, chronic myelogenous leukaemia,
 CC cancer, liver disease, Hodgkin's disease, Lyme's disease, cachexia,
 CC autoimmune diabetes or systemic lupus erythematosus. This is the amino
 CC acid sequence of mouse TANGO-93

XX Sequence 156 AA;

Query Match 100.0%; Score 156; DB 7; Length 156;
 Best Local Similarity 100.0%; Pred. No. 4.2e-159;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVYL 60
 DB 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVYL 60
 OY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
 DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
 OY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDIFYFOCCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDIFYFOCCD 156

RESULT 6
 ADJ88315
 ID ADJ88315 standard; protein; 156 AA.

AC ADJ88315;

DT 06-MAY-2004 (first entry)

DE Mouse interleukin-1delta protein.

XX Interleukin-1zeta; gene therapy; immune system; haematopoietic cell;
 KW inflammatory disorder; infection; allergy; cancer; mouse.

OS Mus musculus.

PN US6680380-B1.

PD 20-JAN-2004.

PF 17-SEP-1999; 99US-00398412.

PR 18-SEP-1998; 98US-0100948P.

XX (SCHE) SCHERING CORP.

PI Timans JC;

XX WPI; 2004-189656/18.

PT New nucleic acid molecules encoding mammalian interleukin-1 polypeptides,
 PT useful for diagnosing, preventing or treating diseases associated with
 PT abnormal expression of interleukin, e.g. inflammation, infection or
 PT cancer.

XX Disclosure; SEQ ID NO 13; 36pp; English.

CC The invention relates to an isolated or recombinant nucleic acid encoding

CC interleukin-1zeta polypeptide. The invention is useful in gene therapy.
 CC The composition and methods are useful in diagnosing or treating
 CC degenerative or abnormal conditions which directly or indirectly involve
 CC development, differentiation or function, e.g. of the immune system
 CC and/or haematopoietic cells. The invention may also be used for
 CC preventing or treating other diseases or disorders associated with
 CC abnormal expression or triggering of response to the interleukin, such as
 CC inflammatory disorders, infection, allergies or cancer. The present
 CC sequence is mouse interleukin-1delta.

XX Sequence 156 AA;

Query Match 100.0%; Score 156; DB 8; Length 156;
 Best Local Similarity 100.0%; Pred. No. 4.2e-159;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVYL 60
 DB 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASISPVYL 60
 OY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
 DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGW 120
 OY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDIFYFOCCD 156
 DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDIFYFOCCD 156

RESULT 7
 ADO04688
 ID ADO04688 standard; protein; 156 AA.

AC ADO04688;

DT 29-JUL-2004 (first entry)

DE Mouse interleukin-1d.

XX Interleukin-1d; IL-1d; immune system; inflammatory reaction;
 KW immunological disorder; mouse.

OS Mus sp.

XX Location/Qualifiers

FT Key 16
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 32
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 48
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 64
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 80
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 96
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 112
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 128
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

FT Misc-difference 144
 FT /note= "Represented by incomplete 3-letter code in
 FT sequence listing"

PN US2004087766-A1.
 XX
 PD 06-MAY-2004.
 XX
 PF 27-OCT-2003; 2003US-00694978.
 XX
 PR 18-SEP-1998; 98US-0100948P.
 PR 17-SEP-1999; 99US-00398412.
 XX
 PA (TIMA/) TIMANS J C.
 XX
 PI Timans JC;
 XX
 DR WPI, 2004-374758/35.
 XX
 PT New isolated or recombinant interleukin-1 zeta polypeptide and related
 PT reagents such as antibodies, useful for treating inflammatory disease and
 PT as probes for diagnosing immunological disorders.
 XX
 PS Disclosure; SEQ ID NO 13; 42pp; English.
 XX
 CC The invention relates to interleukin-1 zeta polypeptide and
 CC polynucleotide. The agonist or antagonist of the interleukin-1 zeta is
 CC useful in modulating a cell that is involved in inflammatory response.
 CC The peptide fragments of IL-1 zeta are useful in research and diagnostic
 CC tools in the study of inflammatory reactions to antigenic challenge and
 CC the development of more effective anti-inflammatory therapeutics.
 CC Interleukin-1 zeta is useful in regulation and/or development of immune
 CC system. A polynucleotide encoding IL-1 zeta is useful for detecting the
 CC expression level of the polypeptide in a patient suspected of having an
 CC immunological disorder. The present sequence is mouse interleukin-1d.
 CC Note: The present sequence is shown in Sequence Listing and pages 6-7 of
 CC the specification. However, the sequence given in sequence listing has
 CC incomplete 3-letter codes for several amino acids.
 XX
 SQ Sequence 156 AA;
 Query Match 100.0%; Score 156; DB 8; Length 156;
 Best Local Similarity 100.0%; Pred. No. 4.2e-159;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVLSGALCFRMDKSAKLVLYLHNNQLLAGLHAKEKVKGBEISVVPNRALDASLSPVIL 60
 DB 1 MMVLSGALCFRMDKSAKLVLYLHNNQLLAGLHAKEKVKGBEISVVPNRALDASLSPVIL 60
 QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYLGAKEKSKFTFYRRDMGLTSSFESAAYPGW 120
 DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYLGAKEKSKFTFYRRDMGLTSSFESAAYPGW 120
 QY 121 FLCTSPPADQPVRLTQIPEDPAMDAPITDIFYFOQCD 156
 DB 121 FLCTSPPADQPVRLTQIPEDPAMDAPITDIFYFOQCD 156
 RESULT 8
 ADQ98213
 ID ADQ98213 standard; protein; 156 AA.
 XX
 AC ADQ98213;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Mouse TANGO-93.
 XX
 KW mouse; TANGO-93; asthma; graft-versus-host disease; rheumatoid arthritis;
 KW psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis;
 KW Crohn's disease; chronic myelogenous leukemia; cancer; liver disease;
 KW Hodgkin's disease; osteoarthritis; Lyme disease; cachexia;
 KW autoimmune disease; myasthenia gravis; autoimmune diabetes;
 KW systemic lupus erythematosus.
 XX
 OS Mus sp.
 XX

PN US2004142420-A1.
 XX
 PD 22-JUL-2004.
 XX
 PF 12-DEC-2003; 2003US-00734985.
 XX
 PR 07-AUG-1998; 98US-00131263.
 PR 06-AUG-1999; 99US-00369693.
 PR 29-APR-2002; 2002US-00134410.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Pan Y;
 XX
 DR WPI, 2004-579909/56.
 DR N-PSDB; ADQ98212.
 XX
 PT New isolated TANGO-93 nucleic acids and proteins, useful for diagnosing,
 PT screening, or treating asthma, rheumatoid arthritis, psoriasis,
 PT inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's
 PT disease, cancer, or liver disease.
 XX
 PS Claim 8; SEQ ID NO 2; 39pp; English.
 XX
 CC The invention relates to an isolated TANGO-93 nucleic acid. The nucleic
 CC acids and polypeptides are useful for diagnosing, screening, or treating
 CC disorders having an aberrant TANGO-93 activity or expression. Diseases
 CC include asthma, graft-versus-host disease, rheumatoid arthritis,
 CC psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis,
 CC Crohn's disease, chronic myelogenous leukemia, cancer, liver disease,
 CC Hodgkin's disease, osteoarthritis, Lyme disease, cachexia, or autoimmune
 CC disease, e.g., myasthenia gravis, autoimmune diabetes, or systemic lupus
 CC erythematosus. The present sequence represents the amino acid sequence of
 CC mouse TANGO-93.
 XX
 SQ Sequence 156 AA;
 Query Match 100.0%; Score 156; DB 8; Length 156;
 Best Local Similarity 100.0%; Pred. No. 4.2e-159;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMVLSGALCFRMDKSAKLVLYLHNNQLLAGLHAKEKVKGBEISVVPNRALDASLSPVIL 60
 DB 1 MMVLSGALCFRMDKSAKLVLYLHNNQLLAGLHAKEKVKGBEISVVPNRALDASLSPVIL 60
 QY 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYLGAKEKSKFTFYRRDMGLTSSFESAAYPGW 120
 DB 61 GVGGSGQCLSCGTEKGPILKLEPVNIMELYLGAKEKSKFTFYRRDMGLTSSFESAAYPGW 120
 QY 121 FLCTSPPADQPVRLTQIPEDPAMDAPITDIFYFOQCD 156
 DB 121 FLCTSPPADQPVRLTQIPEDPAMDAPITDIFYFOQCD 156
 RESULT 9
 AAY96937
 ID AAY96937 standard; protein; 155 AA.
 XX
 AC AAY96937;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Murine IL-1 receptor antagonist 3.
 XX
 KW mIL-1Ra3; interleukin-1 receptor antagonist-3; IL-1ip; osteopathic;
 KW interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
 KW anti-arthritis; antimicrobial; respiratory; anti-ischemic; vaccine;
 KW dermatological; immunomodulatory; gastrointestinal; gene therapy.
 XX
 OS Mus sp.
 XX
 PN WO200039297-A2.
 XX

PD 06-JUL-2000.
XX
XX 22-DEC-1999; 99WO-US030720.
XX
XX 23-DEC-1998; 98US-0113430P.
PR 22-JAN-1999; 99US-0116843P.
PR 13-APR-1999; 99US-0129122P.
XX
XX (GETH) GENENTECH INC.
XX
PI Goddard A, Pan J;
XX
XX WPI, 2000-452395/39.
DR N-PSDB; AAA51599.
XX
XX Nucleic acids encoding interleukin-1-like polypeptides, useful for
PT preventing and treating e.g. inflammation, asthma and psoriasis.
XX
XX Claim 22; Fig 9A-B; 143pp; English.
XX
XX An isolated nucleic acid molecule encoding an interleukin-1-like
CC polypeptide (IL-11p) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (IL-1Ra1) polypeptide, is new. The
CC nucleic acid may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-11p polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patient's production of the polypeptide or to rectify
CC mutations that lead to the production of an active peptide). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-11p protein expression and activity which may be used
CC to treat disorders associated with inappropriate IL-11p expression and
CC activity, such as inflammatory disorders, asthma, arthritis, distress
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC psoriasis, graft versus host disease and/or inflammatory bowel disease
XX
XX Sequence 155 AA;
SQ
Query Match 99.4%; Score 155; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. Se-158;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 MYLSGALCFRMDKSAKLYLHNNQLAGGLHAERKVIKGEISVVPNRALDASLSPVILG 61
DB 1 MYLSGALCFRMDKSAKLYLHNNQLAGGLHAERKVIKGEISVVPNRALDASLSPVILG 60
QY 62 VOGSGQCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGMF 121
DB 61 VOGSGQCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGMF 120
QY 122 LCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 LCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 155
RESULT 10
AAB66672
ID AAB66672 standard; protein, 155 AA.
XX
XX AAB66672;
AC
XX
XX 05-APR-2001 (first entry)
DT
XX
XX Invention related sequence #4.
DE
XX
XX Interleukin, IL-1 receptor; cancer; inflammation.
KW
XX
XX Mus sp.
OS
XX
XX WO200102571-A2.
PN

XX
XX 11-JAN-2001.
XX
XX 07-JUL-2000; 2000WO-US018710.
XX
XX 07-JUL-1998; 99US-00348942.
PR 13-OCT-1999; 99US-00417455.
PR 08-DEC-1999; 99US-00457626.
PR 10-MAR-2000; 2000US-00523552.
PR 22-MAY-2000; 2000US-00576008.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Ford J, Pace A;
PI
XX
XX WPI, 2001-071582/08.
XX
XX Isolated nucleic acids encoding interleukin-1 (IL-1) receptor antagonist
PT proteins (referred as IL-1HY1), useful in the treatment of cancer, e.g.
PT breast adenocarcinoma and brain tumors, and an inflammatory disease
PT mediated by IL-18.
XX
XX Disclosure; Page 177; 179pp; English.
XX
XX The present invention relates to interleukin (IL)-1 receptor antagonist
CC proteins. IL-1HY1 is useful for treating cancer, an inflammatory disease
CC mediated by IL-18, inflammation resulting from infection or allergic
CC reactions, and inflammation associated with chronic bronchitis,
CC arthritis, diabetes or endothermia
XX
XX Sequence 155 AA;
SQ
Query Match 99.4%; Score 155; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. Se-158;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 MYLSGALCFRMDKSAKLYLHNNQLAGGLHAERKVIKGEISVVPNRALDASLSPVILG 61
DB 1 MYLSGALCFRMDKSAKLYLHNNQLAGGLHAERKVIKGEISVVPNRALDASLSPVILG 60
QY 62 VOGSGQCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGMF 121
DB 61 VOGSGQCLSCGTEKGPILKLEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGMF 120
QY 122 LCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
DB 121 LCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 155
RESULT 11
AAB48828
ID AAB48828 standard; protein, 155 AA.
XX
XX AAB48828;
AC
XX
XX 09-MAR-2001 (first entry)
DT
XX
XX Murine interleukin-1 homologue 3 (IL-1H3).
DE
XX
XX Interleukin-1 homologue 3; IL-1H3; mouse; murine; drug screening;
KW agonist; antagonist; human disease; chronic inflammation;
KW acute inflammation; septicemia; autoimmune disease; psoriasis;
KW inflammatory bowel disease; arthritis; transplant rejection; infection;
KW graft versus host disease; acute respiratory distress syndrome; allergy;
KW asthma; restenosis; stroke; ischaemia; brain injury; AIDS; bone disease;
KW osteoporosis; cancer; lymphoproliferative disorder; atherosclerosis;
KW congestive heart failure; Alzheimer's disease; immunosuppressive;
KW antimicrobial; neuroprotective.
XX
XX Mus musculus.
OS
XX
XX WO200071583-A1.
PN

PD 30-NOV-2000.
 XX 24-MAY-2000; 2000WO-US014200.
 XX 24-MAY-1999; 99US-0135599P.
 PR 23-MAY-2000; 2000US-00577715.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Smith RF, Young PR, McDonnell PC, Halsey W;
 PI WPI: 2001-025138/03.
 DR N-PSDB; AAC81700.
 XX Murine interleukin-1 homolog polypeptide used for screening modulators of
 PT the polypeptide which can be used for treating autoimmune diseases,
 PS cancer, brain injury and bone disorders.
 XX Claim 2; Page 28-29; 31pp; English.
 CC The invention relates to murine interleukin-1 homologue 3 (IL-1H3;
 CC AAB48828) and nucleic acids which encode it (cDNA given in AAC81700),
 CC including nucleic acid sequences with at least 95% identity to AAC81700.
 CC The invention also relates to expression vectors and host cells
 CC comprising murine IL-1H3 nucleic acids, the recombinant production of
 CC murine IL-1H3, methods of screening for modulators of IL-1H3 activity,
 CC and IL-1H3 agonists and antagonists thus identified. IL-1H3 agonists and
 CC antagonists are of use for treating human diseases such as chronic or
 CC acute inflammation, septicemia, autoimmune diseases (e.g., inflammatory
 CC bowel disease, psoriasis and arthritis), transplant rejection, graft
 CC versus host disease, infection, stroke, ischaemia, acute respiratory
 CC distress syndrome, allergies, asthma, restenosis, brain injury, AIDS,
 CC bone diseases (e.g., osteoporosis), cancers (e.g., lymphoproliferative
 CC disorders), congestive heart failure, atherosclerosis and Alzheimer's
 CC disease. The present sequence represents murine IL-1H3
 CC
 SQ Sequence 155 AA;
 Query Match 99.4%; Score 155; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 5e-158;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MVLGALCFPMKDSALKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASLPVILG 61
 DB 1 MVLGALCFPMKDSALKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASLPVILG 60
 QY 62 VGGSGQCLSCGTEKGPILKLEPNVIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 121
 DB 61 VGGSGQCLSCGTEKGPILKLEPNVIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 120
 QY 122 LCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCD 156
 DB 121 LCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCD 155
 RESULT 12
 AAB35261
 ID AAB35261 standard; protein; 155 AA.
 XX AAB35261;
 AC 08-MAY-2001 (first entry)
 DT 08-MAY-2001 (first entry)
 XX Murine IL-1L1.
 DE Mouse; IL-1L1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;
 KM chromosome 2q13; inflammatory disease; heart disease; Graves' disease;
 KM rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;
 KM osteoporosis; systemic lupus erythematosus.
 XX Mus sp.
 OS
 XX

PN W0200105974-A2.
 XX 25-JAN-2001.
 PD 17-JUL-2000; 2000WO-US019508.
 XX 16-JUL-1999; 99US-0144298P.
 XX (INTE-) INTERLEUKIN GENETICS INC.
 PA Nicklin M, Barton J;
 PI WPI: 2001-091974/10.
 DR Nucleic acids encoding human and murine interleukin-1L1 polypeptides
 PT useful for controlling inflammatory processes.
 PS Claim 11; Fig 3; 150pp; English.
 CC The present invention provides the protein and coding sequences of the
 CC human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is
 CC located between the IL-1beta and IL-1receptor genes at human chromosome
 CC 2q13. The sequences are useful in the diagnosis, prevention and treatment
 CC of heart disease, cancer and inflammatory diseases such as rheumatoid
 CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,
 CC diabetes, psoriasis, osteoporosis, lichen sclerosus, ulcerative colitis,
 CC severe periodontal disease and pregnancy complications. The present
 CC sequence is the murine IL-1L1 protein
 CC
 SQ Sequence 155 AA;
 Query Match 99.4%; Score 155; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 5e-158;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MVLGALCFPMKDSALKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASLPVILG 61
 DB 1 MVLGALCFPMKDSALKVLYLHNNQLAGGLHAKEVYKGEISVVPNRALDASLPVILG 60
 QY 62 VGGSGQCLSCGTEKGPILKLEPNVIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 121
 DB 61 VGGSGQCLSCGTEKGPILKLEPNVIMELYGAKESKSFYRRDMGLTSSPESAAYPGW 120
 QY 122 LCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCD 156
 DB 121 LCTSPBADQPVRLTQIPEDPAMDAPITDFFFOCD 155
 RESULT 13
 AAB06663
 ID AAB06663 standard; protein; 154 AA.
 XX AAB06663;
 AC 16-OCT-2001 (first entry)
 DT 16-OCT-2001 (first entry)
 XX Mouse interleukin-1delta (IL-1delta) protein.
 DE Mouse; interleukin-1delta; IL-1delta; viruslike; hepatotropic; fever;
 KM immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
 KM autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
 KM psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
 XX Mus sp.
 OS
 XX W0200157219-A2.
 PN 09-AUG-2001.
 PD 01-FEB-2001; 2001WO-US003285.
 XX 02-FEB-2000; 2000US-0179638P.
 XX

PA (SCHE) SCHERING CORP.
 XX Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
 PI WPI, 2001-488886/53.
 XX
 DR Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
 PT polypeptide useful for treating conditions exhibiting abnormal expression
 PT of interleukin such as immunological disorders, tumor and allergy.
 XX
 PS Disclosure; Fig 1, 103pp; English.
 XX
 XX The invention relates to recombinant antigenic interleukin-1 like
 CC molecules and their corresponding nucleic acid sequences, designated as
 CC interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon). IL
 CC -1delta and IL-1epsilon are useful for treating conditions exhibiting
 CC abnormal expression of the interleukin such as immunological disorders,
 CC tumors, inflammatory disorders, fever, hypoglycaemia, psoriasis,
 CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
 CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
 CC HIV). The invention also relates to methods of using the composition
 CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
 CC utilities. IL-1delta is used as an immunogen for the production of
 CC antisera or antibodies specific, e.g., capable of distinguishing between
 CC IL-1 family members and an IL-1delta, for the interleukin or its
 CC fragment. The purified interleukin is used as a reagent to detect any
 CC antibodies generated in response to the presence of elevated levels of
 CC expression, or immunological disorders which lead to antibody production
 CC to the endogenous cytokine. The invention also contemplates the use of
 CC competitive drug screening assays. The present sequence is mouse
 CC interleukin-1delta (IL-1delta) protein related to the invention
 SQ
 Sequence 154 AA;
 Query Match 98.7%; Score 154; DB 4; Length 154;
 Best Local Similarity 100.0%; Pred. No. 5.9e-157; Indels 0; Gaps 0;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 VLSGALCFPMKDSALKVLYLHNNQLAGLHAERIVKGEISVVPNRALDASIPVILGV 62
 DB 1 VLSGALCFPMKDSALKVLYLHNNQLAGLHAERIVKGEISVVPNRALDASIPVILGV 60
 QY 63 QGSGOCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWFL 122
 DB 61 QGSGOCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWFL 120
 QY 123 CTSPEADQPVRLTQIPEDPAMDAPIIDFYFOOD 156
 DB 121 CTSPEADQPVRLTQIPEDPAMDAPIIDFYFOOD 154
 RESULT 14
 ABP52012
 ID ABP52012 standard; protein, 146 AA.
 XX
 AC ABP52012;
 XX
 DT 10-OCT-2002 (first entry)
 XX
 DE NOVINTRA A homologous amino acid sequence SEQ ID NO:55.
 XX
 XX Human; transmembrane protein; neuromedin protein; gonadotropin protein;
 KW interleukin-1 receptor antagonist; interleukin-1 epsilon; NOVY;
 KW IL-1 epsilon; IL-1 receptor antagonist; lung disease; neutropenic;
 KW cytotoxic; neuroprotective; antiinflammatory; antibacterial;
 KW immunosuppressive; cerebroprotective; antidiabetic; antiarthritic;
 KW antiasthmatic; antiallergic; gene therapy; antibody-based therapy;
 KW cell signalling disorder; haematopoietic disorder; endocrine; muscle;
 KW neurodegenerative disorder; neurolgical disorder; cancer; melanoma;
 KW central nervous system cancer; reproductive development disorder; asthma;
 KW metabolic function disorder; bone metabolism; structure disorder; stroke;
 KW inflammatory response disorder; immune regulation disorder; septic shock;
 KW diabetes; arthritis; lung cancer; emphysema; allergic lung irritation;

KW lung inflammation.
 XX Homo sapiens.
 OS US2002068279-A1.
 XX
 PN 06-JUN-2002.
 PD 05-DEC-2000; 2000US-00730617.
 PF 06-DEC-1999; 99US-0169056P.
 PR 09-DEC-1999; 99US-0169866P.
 PR 09-DEC-1999; 99US-0169866P.
 PR 10-DEC-1999; 99US-0170252P.
 PR 12-JAN-2000; 2000US-0175740P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 XX Burgess C, Prayaga SK, Shimkets RA, Rastelli L, Zernusen B;
 PI Mezes P;
 DR WPI, 2002-582472/62.
 XX
 PT New NOVX proteins for diagnosing or treating cell signaling, immune
 PT response, hematopoietic, neurodegenerative, muscle, endocrine, bone, and
 PT reproductive development disorders.
 PS Disclosure; Fig 10B, 110pp; English.
 XX
 XX The present invention describes an isolated NOVX polypeptide, chosen from
 CC human transmembrane (NOVTRAN), neuromedin (NOVNEUR), gonadotropin
 CC (NOVGON), interleukin-1 (IL-1) receptor antagonist (NOVINTRA A and B),
 CC and IL-1 epsilon proteins. NOVX polypeptides have neutropenic, cytotoxic,
 CC neuroprotective, antiinflammatory, antibacterial, immunosuppressive,
 CC cerebroprotective, antidiabetic, antiarthritic, antiasthmatic and
 CC antiallergic activities, and can be used in gene therapy and antibody-
 CC based therapy. NOVX polypeptides, nucleic acid (I) encoding them and an
 CC antibody (III) that binds the polypeptide, are useful for treating or
 CC preventing a NOVX protein-associated disorder in humans. NOVTRAN can be
 CC used in the treatment of a cell signalling disorder, such as, a
 CC haematopoietic disorder or a neurodegenerative disorder. NOVNEUR can be
 CC used in the treatment of an endocrine, muscle, neurological disorder,
 CC central nervous system cancer, breast, colon, ovarian, kidney, prostate
 CC or thyroid cancer. NOVGO can be used in the treatment of a reproductive
 CC development disorder, metabolic function disorder or melanoma. NOVINTRA
 CC proteins can be used in the treatment of a bone metabolism or
 CC structure disorder, an inflammatory response disorder, an immune
 CC regulation disorder, septic shock, stroke, diabetes, arthritis or cancer.
 CC An agent which modulates the expression or activity of a human IL-1
 CC epsilon protein is useful for treating a lung disease such as lung
 CC cancer, asthma, emphysema, allergic lung irritation and lung inflammation
 CC in a mammal. ABQ73996 to ABQ74027 and ABP51981 to ABP52048 represent
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 146 AA;
 Query Match 93.6%; Score 146; DB 5; Length 146;
 Best Local Similarity 100.0%; Pred. No. 2.3e-148; Indels 0; Gaps 0;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 CFRMDSALKVLYLHNNQLAGLHAERIVKGEISVVPNRALDASIPVILGVGGSGOC 68
 DB 1 CFRMDSALKVLYLHNNQLAGLHAERIVKGEISVVPNRALDASIPVILGVGGSGOC 60
 QY 69 LSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWFLCTSPEA 128
 DB 61 LSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWFLCTSPEA 120
 QY 129 DQPVRLTQIPEDPAMDAPIIDFYFOO 154
 DB 121 DQPVRLTQIPEDPAMDAPIIDFYFOO 146

Search completed: April 5, 2006, 15:10:21
Job time : 82 secs

```

RESULT 15
AA97068
ID AAY97068 standard; protein, 94 AA.
XX
XX AC AAY97068;
XX
XX DT 31-OCT-2000 (first entry)
XX
DE Murine IL-1 receptor antagonist 3 EST W08205 product.
XX
XX mIL-1Ra3; interleukin-1 receptor antagonist-3; IL-1p; osteopathic;
XX interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
XX anti-arthritic; antimicrobial; respiratory; anti-ischemic; vaccine;
XX dermatological; immunomodulatory; gastrointestinal; gene therapy.
XX
OS Mus sp.
XX
XX PN W0200039297-A2.
XX
XX PD 06-JUL-2000.
XX
XX PF 22-DEC-1999; 99WO-US030720.
XX
XX PR 23-DEC-1998; 98US-0113430P.
XX PR 22-JAN-1999; 99US-0116843P.
XX PR 13-APR-1999; 99US-0129122P.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Goddard A, Pan J;
XX
XX DR WPI; 2000-452395/39.
XX DR N-PSDB; AAA51600.
XX
XX PT Nucleic acid encoding interleukin-1-like polypeptides, useful for
XX PT preventing and treating e.g. inflammation, asthma and psoriasis.
XX
XX PS Example 1; Fig 10; 143pp; English.
XX
XX CC An isolated nucleic acid molecule encoding an interleukin-1-like
XX CC polypeptide (IL-1p) that retains one or more activities of the peptide
XX CC from which it is derived, such as the IL-18R binding activity of a human
XX CC interleukin-1 receptor antagonist-1 (hIL-1Ra1) polypeptide, is new. The
XX CC nucleic acids may be used in molecular engineering applications, e.g.
XX CC hybridization assays and chromosome and gene mapping studies, for
XX CC recombinantly producing the IL-1p polypeptide or for producing gene
XX CC knock out animals to study the role of the protein in metabolism and
XX CC disease processes (conversely, gene therapy protocols may be used to
XX CC supplement a patient's production of the polypeptide or to rectify
XX CC mutations that lead to the production of in active peptides). The
XX CC peptides produced may be used to screen for and produce modulators (e.g.
XX CC antibodies) of IL-1p protein expression and activity which may be use to
XX CC treat disorders associated with inappropriate IL-1p expression and
XX CC activity, such as inflammatory disorders, asthma, arthritis,
XX CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
XX CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
XX CC psoriasis, graft versus host disease and/or inflammatory bowel disease
XX
SQ Sequence 94 AA;

Query Match          60.3%; Score 94; DB 3; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.3e-92;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMTLSGALCFRMDSALKVLYLNNOULAGLHAKEVYKGEESVVPNALDASLSPVIL 60
DB 1 MMTLSGALCFRMDSALKVLYLNNOULAGLHAKEVYKGEESVVPNALDASLSPVIL 60
QY 61 GVOGGSQCLSCGTEKGPILKLEPVNIMELYIAK 94
DB 61 GVOGGSQCLSCGTEKGPILKLEPVNIMELYIAK 94

```

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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:10:32 ; Search time 14 Seconds

(without alignments)
1072.130 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 156
Sequence: 1 MAMLSGALCFRMKDSALKVL.....IPEDPAMDAPITDFYFOQCD 156

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 8

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 80.*

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	28.2	155	2 JC7104	Interleukin-1 rece
2	9	5.8	413	2 T05228	hypothetical prote
3	8	5.1	196	2 AH1149	hypothetical prote
4	8	5.1	196	2 A11508	hypothetical prote
5	8	5.1	883	2 T37208	hypothetical prote

ALIGNMENTS

RESULT 1

JC7104 Interleukin-1 receptor antagonist - human

C/Species: Homo sapiens (man)
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: JC7104
R/Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford, D.

Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A/Title: IL1RI1: A novel interleukin-1 receptor antagonist gene.

A/Reference number: JC7104; MUID:99443727; PMID:10512743

A/Accession: JC7104
A/Molecule type: mRNA

A/Residues: 1-155 <MUL>
A/Cross-references: UNIPROT:Q9UBH0; UNIPARC:UP10000034E98; GB:AF186094; NID:96049804; PI

C/Genetics:

A/Map position: 2q14

C/Keywords: macrophage

Query Match 28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 4.3e-39;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 LEPNIMELYGAKEKSPFTYRRDMLGTSSPSSAAYRGWFLCT 124
DB 80 LEPNIMELYGAKEKSPFTYRRDMLGTSSPSSAAYRGWFLCT 123

RESULT 2

T05228 hypothetical protein F1715.190 - Arabidopsis thaliana

N/Alternate names: Hypothetical protein F28A23.240
C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C/Accession: T05228; T05436
R/Bevan, M.; Vitale, D.; Ligunori, R.; Argitrou, A.; De Simone, V.; Hohnsbeil, J.; Mew

submitted to the Protein Sequence Database, July 1998
A/Reference number: Z15404

A/Accession: T05228
A/Molecule type: DNA

A/Residues: 1-413 <BEV>
A/Cross-references: UNIPROT:Q49504; UNIPARC:UP100000A0329; EMBL:AL031032

A/Experimental source: cultivar Columbia; BAC clone F1715
R/Bevan, M.; Weichselgartner, M.; Fattmann, B.; Grandérach, K.; Dauner, D.; Herzl, A.

submitted to the Protein Sequence Database, October 1998
A/Reference number: Z15415

A/Accession: T05436
A/Molecule type: DNA

A/Residues: 173-413 <BEV>
A/Cross-references: UNIPARC:UP1000017A66F; EMBL:AL021961

A/Experimental source: cultivar Columbia; BAC clone F28A23
C/Genetics:

A/Map position: 4
A/Intons: 306/3

A/Note: F1715.190; F28A23.240

Query Match 5.8%; Score 9; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ALDASLSPV 58
DB 356 ALDASLSPV 364

RESULT 3

AH1149 hypothetical protein lmo0600 [imported] - Listeria monocytogenes (strain EGD-e)

C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: AH1149
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Feibi,

D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001

A/Authors: Kreft, U.; Kuhn, M.; Kunet, F.; Kurapkat, G.; Madueno, E.; Maloum, A.;
Ok, C.; Schlatter, T.; Simoes, N.; Tixeret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla

A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: AH1149
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-196 <GLA>

A/Cross-references: UNIPROT:O8Y9D2; UNIPARC:UP1000005526; GB:NC_003210; PIDN:CAC9867
A/Experimental source: strain EGD-e
C/Genetics:

A/Note: lmo0600

Query Match 5.1%; Score 8; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 LSPVILGV 62
 |||||
 Db 130 LSPVILGV 137

RESULT 4

hypoetical protein lin0609 [imported] - Listeria innocua (strain Clp11262)
 A11508
 C:Species: Listeria innocua
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: A11508
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baguerio, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karsc, U.
 Science 294, 849-852, 2001
 A:Authors: Kref, J.; Kuhn, M.; Kunat, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.; Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: A11508
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-196 <GLA>
 A:Cross-references: UNIPROT:Q92E52; UNIPARC:UPI00000CC2B8; GB:AL592022; PIDN:CAC95841.1;
 A:Experimental source: strain Clp11262
 C:Genetics:
 A:Gene: lin0609

Query Match 5.1%; Score 8; DB 2; Length 196;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 LSPVILGV 62
 |||||
 Db 130 LSPVILGV 137

RESULT 5

T37208
 hypoetical protein Y57G7A.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T37208
 R:Ozerky, P.
 submitted to the EMBL Data Library, March 1999
 A:Description: The sequence of C. elegans cosmid Y57G7A.
 A:Reference number: Z21634
 A:Accession: T37208
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-883 <OZE>
 A:Cross-references: UNIPROT:O76623; UNIPARC:UPI0000076054; EMBL:AF077542; PIDN:AA026299.
 C:Genetics:
 A:Map position: II
 A:introns: 20/1; 47/1; 756/2; 822/2; 852/1
 A>Note: Y57G7A.6

Query Match 5.1%; Score 8; DB 2; Length 883;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86 IMELYLGA 93
 |||||
 Db 231 IMELYLGA 238

Search completed: April 5, 2006, 15:10:54
 Job time : 14 secs

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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:09:00 ; Search time 77 Seconds

(without alignments)
1429.382 Million cell updates/sec

Title: US-09-770-528-2

Sequence: 1 MMTLSGALCFRMKDSALKVL.....IPEDPAMDAPITDFYFQOCD 156

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 8

Total number of hits satisfying chosen parameters: 27

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*
2: uniprot_tramb1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	156	100.0	156	ILIF5_MOUSE	O99Y1 mus musculu
2	44	28.2	155	ILIF5_HUMAN	Q9UBH0 h interlex
3	10	6.4	104	OSACR2_CANAL	OSACR2 candida alb
4	9	5.8	382	OSTS48_ANOGA	OSTS48 anopheles g
5	9	5.8	413	049504_ARATH	049504 arabidopsis
6	9	5.8	449	09C501_ARATH	09C501 arabidopsis
7	9	5.8	454	09M703_ARATH	09M703 arabidopsis
8	8	5.1	101	070AK0_XENTR	070AK0 xenopus tro
9	8	5.1	110	070AK1_XENTR	070AK1 xenopus lae
10	8	5.1	174	ILIRA_BOVIN	077482 bos taurus
11	8	5.1	196	08Y9D2_LISMO	08Y9D2 listeria mo
12	8	5.1	196	092ES2_LISIN	092ES2 listeria in
13	8	5.1	196	0722V0_LISIN	0722V0 listeria mo
14	8	5.1	263	06E4C0_PETMA	06E4C0 petromyzon
15	8	5.1	278	06ETX4_ORYSA	06ETX4 oryza sativ
16	8	5.1	397	0877R1_BACTIN	0877R1 bacteroides
17	8	5.1	570	070AK2_XENTR	070AK2 xenopus lae
18	8	5.1	581	09D505_MOUSE	09D505 m mus muscu
19	8	5.1	590	09D2F4_MOUSE	09D2F4 m mus muscu
20	8	5.1	620	04QF97_LEIMA	04QF97 leishmania
21	8	5.1	637	06A073_MOUSE	06A073 mus musculu
22	8	5.1	660	FLR12_HUMAN	043155 homo sapien
23	8	5.1	660	08BLU0_MOUSE	08BLU0 mus musculu
24	8	5.1	673	07Y258_CHURE	07Y258 chlamydomon
25	8	5.1	883	076623_CABEL	076623 caenorhabdi
26	8	5.1	3365	06XRA7_DICHI	06XRA7 dictyosceli
27	8	5.1	4780	05CRB3_CRYPY	05CRB3 cryptospori

ALIGNMENTS

RESULT 1
ID ILIF5_MOUSE STANDARD; PRT; 156 AA.
AC O99Y1; O9YIG2;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin 1 family member 5 (IL-1F5) (Interleukin-1 delta) (IL-1
DE delta) (Interleukin-1-like protein 1) (IL-1L1) (Interleukin-1 HX1)
DE (IL-1H1) (Interleukin-1 homolog 3) (IL-1H3).
GN Name:ILIF5; Synonyms:Flid, Ilth3, Ilthyl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20545212; PubMed=11466363;
RX Debets R., Timas J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
RA Kastelein R.A.;
RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
RT as an antagonist and agonist of NF-kappa B activation through the
RT orphan IL-1 receptor-related protein 2.";
RL J. Immunol. 167:1440-1446(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20545212; PubMed=11093146;
RX DOI=10.1002/1521-4141(200111)30:11<3299::AID-IMUJ3299>3.0.CO;2-S;
RA Barton J.L., Herbst R., Bossio D., Higgins L., Nicklin M.J.H.;
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
RL Eur. J. Immunol. 30:3299-3308(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Timas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX STRAIN=C57BL/6J; TISSUE=Stomach; and Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1098/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
RA Nakai K., Tomaru Y., Hasegawa Y., Nogi H., Yamada I., Kiyosawa H.,
RA Yagi K., Nogi Y., Hasegawa Y., Nogi H., Nogi H., Nogi H., Nogi H.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kampen A., Matsuda H., Barilov S., Baisel K.W.,
RA Blake J.A., Brad T., Brusic V., Chotia C., Corbani L.B., Cousins S.,
RA Dalia E., Dragani T.A., Fletcher C.F., Fortescue A., Fraser K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimsmond S., Gustincich S., Hirokawa N., Jackson J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagawa A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magliotti D.R., Malais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan M.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai K., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid D.J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takemata Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Varadar R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carmichael P., Hayatsu N.,
RA Hirose-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Aizawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RL 60,770 full-length cDNAs.";
 Nature 420:563-573 (2002).
 (5)
 RN X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 3-156, AND DISULFIDE BOND.
 RP PubMed=12974628; DOI=10.1021/bk10341197;
 RA Dunn E.P., Gay N.J., Bristow A.F., Gearing D.P., O'Neill L.A.J.,
 RA Pei X.Y.;
 RT "High-resolution structure of murine interleukin 1 homologue IL-1F5
 RT reveals unique loop conformations for receptor binding specificity.";
 RL Biochemistry 42:10938-10944 (2003).
 CC -1- FUNCTION: Is a highly and a specific antagonist of the IL-1
 CC receptor-related protein 2-mediated response to interleukin 1
 CC family member 9 (IL1P9). Could constitute part of an independent
 CC signaling system analogous to interleukin-1 alpha (IL-1A), beta
 CC (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-
 CC 1R1), that is present in epithelial barriers and takes part in
 CC local inflammatory response (By similarity).
 CC SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly abundant in embryonic tissue and
 CC tissues containing epithelial cells.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AF2030378; AAF91275.1; -; mRNA.
 CC EMBL: AK009741; BAB26471.1; -; mRNA.
 CC EMBL: AK008977; BAB26402.1; -; mRNA.
 CC EMBL: AF2050429; CAB59831.1; ALT. INIT.; mRNA.
 CC EMBL: AF204955; AAF69251.1; -; mRNA.
 CC PDB: 1MD6; X-ray; A=3-156.
 CC Ensembl: ENSMUSG0000026983; Mus musculus.
 CC MGI: MGI:1859325; 111F5.
 CC InterPro: IPR000975; Interleukin 1.
 CC InterPro: IPR003296; Interleukin1LB.
 CC InterPro: IPR003297; Interleukin1LRA.
 CC PANTHER: PTHR10078; SE2; Interleukin1LRA; 1.
 CC Pfam: PF00340; IL1; 1.
 CC PRINTS: PRO0264; INTERLEUKIN1.
 CC PRINTS: PRO1359; INTERLEUKIN1B.
 CC PRINTS: PRO1360; INTERLEUKIN1X.
 CC ProDom: PD002536; Interleukin_1; 1.
 CC SMART: SM00125; IL1; 1.
 CC PROSITE: PS00253; INTERLEUKIN_1; 1.
 CC 3D-structure: Cytochrome; Multigene family.
 CC DISULFID 9
 CC FT 155
 CC CONFLICT 2
 CC SEQUENCE 156 AA; 17136 MW; A4DIE2F93CF77A7 CRC64;
 SQ
 Query Match 100.0%; Score 156; DB 1; Length 156;
 Best Local Similarity 100.0%; Pred. No. 3e-158;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID IL1F5_HUMAN STANDARD; PRT; 155 AA.
 AC OSUBHD; OS6AT9; Q7RTZ6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Interleukin 1 family member 5 (IL-1F5) (Interleukin-1 delta) (IL-1
 DE delta) (F1L1 delta) (Interleukin-1-like protein 1) (IL-1L1)
 DE (Interleukin-1 HX1) (IL-1HX1) (Interleukin-1 receptor antagonist
 DE homolog 1) (IL-1ra homolog 1) (IL-1 related protein 3) (IL-1RP3).
 GN Name=IL1F5; Synonyms=FL1D, IL1H1, IL1L1, IL1RP3;
 GN ORFNames=ONQ1896/PRO4342;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 CC NCB1_Taxid=9606;
 CC (1)
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP TISSUE=placenta;
 RC MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
 RX Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garika K.E.,
 RA Sims J.E.;
 RT "Four new members expand the IL-1 superfamily.";
 RL J. Biol. Chem. 275:1169-1175 (2000).
 (2)
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP TISSUE=retal skin;
 RC MEDLINE=99443727; PubMed=10512743; DOI=10.1006/birc.1999.1440;
 RX Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
 RA Drmanac R., Ford J.E.;
 RT "IL1H1: a novel interleukin-1 receptor antagonist gene";
 RL Biochem. Biophys. Res. Commun. 263:702-706 (1999).
 (3)
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP TISSUE=placenta;
 RC MEDLINE=20545212; PubMed=11093146;
 RX DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
 RA Barton J.L., Herbst R., Bosio D., Higgins L., Nicklin M.J.H.;
 RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
 RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
 RL Eur. J. Immunol. 30:3299-3308 (2000).
 (4)
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP MEDLINE=21359532; PubMed=11466363;
 RX Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
 RA Wagner J., Edwards G., Clifford T., Memon S., Bazan J.F.,
 RA Kastelein R.A.;
 RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
 RT as an antagonist and agonist of NF-kappa B activation through the
 RT orphan IL-1 receptor-related protein 2.";
 RL J. Immunol. 167:1440-1446 (2001).
 (5)
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RP MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
 RX Buefield S.J., Comrack C.A., Yu G., Chikering T.W., Smutko J.S.,
 RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
 RT "Identification and gene organization of three novel members of the
 RT IL-1 family on human chromosome 2.";
 RL Genomics 66:213-216 (2000).
 (6)
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RP MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
 RX Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald W.G., Duff W.G.,
 RA Kornman K.;
 RT "A sequence-based map of the nine genes of the human interleukin-1
 RT cluster.";
 RL Genomics 79:718-725 (2002).
 (7)
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RX Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Dewel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,

RESULT 2
 IL1F5_HUMAN

RA Huang A., Kim H.-S., Klimowski L.B., Jin Y., Johnson S., Lee J.
RA Lewis L., Lim D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.
RA Sebahagiri S., Simmons L., Singh U., Smith V., Stinson J., Vasts A.,
RA Vandlen R.L., Watanabe C., Weiland D., Woods K., Xie M.-H.,
RA Yanusa D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003) .

RN [8]
RP NCBI/GENOTYPE SEQUENCE [GENOMIC DNA], AND VARIANT SER-47.
RA Richter M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Abearn M.O.,
RA Bettucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
RA "ssatlesnpfs, NHUHI H16662 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu)".
RL Submitted (MAR-2005) to the EMBL/GenBank/DDBB databases.

RN [9]
RP NCBI/GENOTYPE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15815621; DOI=10.1038/nature03466.
RA Hillier L.W., Graves T.A., Fulton R.S., Fulton L.A., Pepin K.H.,
RA Minx P., Wagner-McPherson C., Layman D., Wyllie K., Sekhon M.,
RA Becker M.C., Fewell G.A., Delahunty K.D., Miner T.L., Nash W.E.,
RA Kremetzki C., Oddy L., Du H., Sun H., Bradshaw-Cordum H., Ali J.,
RA Grewal N., Goyea E., Hou S., Levy A., Martinica S., Mead K.,
RA McCellan M.D., Meyer R., Randall-Maher J., Tomlinson C.,
RA Daughin-Kohlberg S., Kozlowicz-Reilly A., Shah N.,
RA Swearingen-Shahid S., Snider J., Strong J.T., Thompson J., Yeakum M.,
RA Leonard S., Pearmann C., Trani L., Radonovic M., Waligorski J.E.,
RA Wang C., Rock S.M., Tin-Wollam A.-M., Maupin R., Latreille P.,
RA Wendt M.C., Yang S.-P., Pohl C., Wallis J.W., Spierch J., Bieri T.A.,
RA Berkowicz N., Nelson J.O., Oborone J., Ding L., Meyer R., Sabo A.,
RA Shioda Y., Sinha P., Wohlmann P.E., Cook L.H., Hickendornham M.T.,
RA Eldred J., Williams D., Jones T.A., She X., Ciccarelli F.D.,
RA Izaurralde E., Taylor J., Schmutz J., Myers R.M., Cox D.R., Huang X.,
RA McPherson J.D., Mardis E.R., Clifton S.W., Warren M.C.,
RA Chinnwala A.T., Eddy S.R., Marra M.A., Orchanenko I., Purey T.S.,
RA Miller W., Eichner E.E., Bork P., Suyama M., Torrents D.,
RA Waterston R.H., Wilson R.K.;
RT "Generation and annotation of the DNA sequences of human chromosomes 2
RT and 4.";
RL Nature 434:724-731(2005) .

RN [10]
RP NCBI/GENOTYPE SEQUENCE [LARGE SCALE MENA].
RC TTSSUSE=Placentaria;
RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bucoaw K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchkento L., Marinina K., Farmer A.R., Rubin G.W., Hong L.,
RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Beak S.A., McBryan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzanski S.J., Skalska M., Smalins D.E.,
RA Schmeichl A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Is a highly and a specific antagonist of the IL-1
receptor-related protein 2-mediated response to interleukin 1

	CC	famly member 9 (IL1P9) . Could constitute part of an independent signaling system analogous to interleukin-1 alpha (IL-1A), beta (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-1RI) , that is present in epithelial barriers and takes part in local inflammatory response.
	CC	-I- SUBCELLULAR LOCATION: Secreted.
	CC	-I- TISSUE SPECIFICITY: Predominantly expressed in keratinocytes but not in fibroblasts, endothelial cells or melanocytes. Detected also in the spleen, brain leukocyte and macrophage cell types.
	CC	-I- INDUCTION: By phorbol ester (PMA) and lypopolysaccharide (LPS) treatment in macrophage cell line.
	CC	-I- SIMILARITY: Belongs to the IL-1 family.
	CC	-----
	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - CC the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
	CC	-----
	DR	EMBL; AF201830; AAT25210.1; -; mRNA.
	DR	EMBL; AF186094; AAF02757.1; -; mRNA.
	DR	EMBL; AJ242737; CAB59822.1; -; mRNA.
	DR	EMBL; AJ242738; CAB59823.1; -; mRNA.
	DR	EMBL; AL211338; CAB67704.1; -; Genomic DNA.
	DR	EMBL; AF216893; AAF76981.1; -; Genomicc_DNA.
	DR	EMBL; AF230377; AAF91274.1; -; mRNA.
	DR	EMBL; BN000002; CAD928477.1; -; Genomicc_DNA.
	DR	EMBL; AY359117; AAC09475.1; -; mRNA.
	DR	EMBL; AY972853; AA559031.1; -; Genomicc_DNA.
	DR	EMBL; AC016724; AA114990.1; -; Genomicc_DNA.
	DR	EMBL; BC024747; AAA24747.1; -; mRNA.
	DR	PIR; JC7104; JC7104.
	DR	HSSP; P18510; ILIR.
	DR	SMR; Q9UBH0; 2-155.
	DR	Interact; Q9UBH0; -;
	DR	Ensembl; ENSG00000136695; Homo sapiens.
	DR	HGNc; HGNC:15561; IL1F5.
	DR	MIM; 605507; -;
	DR	GO; GO:0005152; F: Interleukin-1 receptor antagonist activity; TAS.
	DR	InterPro; IPP0000975; Interleukin_1.
	DR	InterPro; IPP003296; InterleukinIL1B.
	DR	InterPro; IPRO03297; InterleukinIL1RA.
	DR	PANTHER; PTR010078; InterleukinIL1RA; 1.
	DR	pfam; PF00340; IL1; 1.
	DR	PRINTS; PRO0264; INTERLEUKIN1.
	DR	PRINTS; PRO1359; INTERLEUKIN1B.
	DR	PRINTS; PRO1360; INTERLEUKIN1X.
	DR	ProDom; PD002536; Interleukin_1; 1.
	DR	SMART; SMO0125; IL1; 1.
	DR	PROSITE; PS00253; INTERLEUKIN_1; 1.
	FT	Cytokine; Multigene family; Polymorphism.
	KW	disulfid 8 154
	VARIANT	47 47 N->S.

	Query Match	28.2%; Score 44; DB 1; Length 155;
	Best Local Similarity	100.0%; Pied. No. 2,6e-38;
	Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	81	LEPVNIMELYLGAKEKSPFFYPRDMGLTSSPESAAYPGGFLLCT 124
Dd	80	LEPVNIMELYLGAKEKSPFFYPRDMGLTSSPESAAYPGGFLLCT 123

	RESULT 3	
	OSACR2 CANAL	
	OSACR2 CANAL PRELIMINARY;	PRT; 104 AA.
	AC OSACR2;	
	DT 10-MAY-2005 (TrEMBLrel. 30, Created)	
	DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)	
	DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)	
	DE Hypothetical protein.	
	DE ORFNames=CaO19..7580;	

OS Candida albicans SC5314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=237561;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SC5314;
 RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
 RA Jones T., Federespiel N.A., Chidana H., Dungan J., Kalman S.,
 RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
 RA Davis R.W., Scherer S.;
 RT "The diploid genome sequence of Candida albicans."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SC5314;
 RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,
 RA Roberts J., Petersen K., Donnelly S., Favoreto S., Tsung K.-W.,
 RA Jones T., Scherer S., Agabian N.;
 RT "Annotation of the Genome of Candida albicans."
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AAC00100032; EAL00454.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 104 AA; 11108 MW; 1879F070BE334FAB CRC64;
 OY 109 TSSFESAAYP 118
 DB 3 TSSFESAAYP 12

Query Match 6.4%; Score 10; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 OSTS48 ANOGA PRELIMINARY; PRT; 382 AA.
 ID OSTS48 ANOGA PRELIMINARY; PRT; 382 AA.
 AC OSTS48;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE ENSANGP0000029593.
 GN ORFNames=ENSANGG0000022974;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae re-annotation."
 RT "Anopheles gambiae re-annotation."
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AAB01008944; EAL40313.1; -; Genomic_DNA.
 KW InterPro; IPR001611; LRR.
 DR InterPro; IPR003885; LRR_cyst.
 DR InterPro; IPR007092; LRR_SDS22.
 DR Pfam; PF00560; LRR_1; 3.
 DR PRINTS; PR00019; LEURICRPT.
 DR SMART; SM00365; LRR_SD22; 4.
 KW Leucine-rich repeat; Repeat.

SQ SEQUENCE 382 AA; 42611 MW; 97D4B319C1D9B647 CRC64;
 OY 19 VLYIANNQL 27
 DB 39 VLYIANNQL 47

Query Match 5.8%; Score 9; DB 2; Length 382;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 O49504 ARATH PRELIMINARY; PRT; 413 AA.
 ID O49504 ARATH PRELIMINARY; PRT; 413 AA.
 AC O49504;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE BZIP transcription factor-like protein.
 GN Name=FL175.190; Synonyms=At4g34000;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Bevan M., Vitale D., Liguori R., Argiriou A., De Simone V.,
 RA Hohnsbeil J., Mewes H.W., Mayer K.F.X., Schueller C.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Vitale D., Liguori R., Argiriou A., De Simone V., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 162-306 AND 307-413.
 RA Weichselgattner M., Partmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031032; CAI19882.1; -; Genomic_DNA.
 DR EMBL; AL161584; CAB80117.1; -; Genomic_DNA.
 DR PIR; T05228; T05228.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; P:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR004827; TF_BZIP.
 DR PROSITE; PS00036; BZIP_BASIC; 1.
 SQ SEQUENCE 413 AA; 44666 MW; C05884DFD45EDD16 CRC64;

Query Match 5.8%; Score 9; DB 2; Length 413;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 O9C501 ARATH PRELIMINARY; PRT; 449 AA.
 ID O9C501 ARATH PRELIMINARY; PRT; 449 AA.
 AC O9C501;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)


```

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BZIP protein DBP5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kim S., Ma J., Li Z., Thomas T.L.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF34210; AAK19603.1; -; mRNA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR011616; bzip 1.
DR InterPro: IPR004827; TF bzip.
DR Pfam: PF00170; bzip 1; 1.
DR SMART: SM00338; BRLZ; 1.
DR PROSITE: PS50217; BZIP; 1.
DR PROSITE: PS00036; BZIP_BASIC; 1.
DR DNA-binding; Nuclear protein.
KW SEQUENCE 449 AA; 48905 MW; 79B7B6B4739872B9 CRC64;

Query Match 5.8%; Score 9; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 ALDASLSPV 58
DB 346 ALDASLSPV 354

RESULT 7
O9MT03 ARATH PRELIMINARY; PRT; 454 AA.
ID O9MT03_
AC O9MT03_
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Abscisic acid responsive elements-binding factor (Hypothetical protein
DE F1715.190:F1715.200) (ABRAB/FAP3).
GN Name=ABRAB; Synonyms=At4g34000, F1715.190:F1715.200;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=20102680; PubMed=1063668; DOI=10.1074/jbc.275.3.1723;
RA Choi H.-I., Hong J.-H., Ha J.-O., Kang J.-Y., Kim S.-Y.;
RA "ABRAB, a family of ABA-responsive element binding factors.";
RL J. Biol. Chem. 275:1723-1730(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.-X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinzaki K.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinzaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.-X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinzaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

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RP NUCLEOTIDE SEQUENCE.
RA Tokoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
RA Narusaka M., Shinn P., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinzaki K.;
RL "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF093546; AAF27181.1; -; mRNA.
DR EMBL: AY054605; AAK96796.1; -; mRNA.
DR EMBL: AY081467; AAM10029.1; -; mRNA.
DR EMBL: AK175851; BAD43614.1; -; mRNA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR011616; bzip 1.
DR InterPro: IPR004827; TF bzip.
DR Pfam: PF00170; bzip 1; 1.
DR SMART: SM00338; BRLZ; 1.
DR PROSITE: PS50217; BZIP; 1.
DR PROSITE: PS00036; BZIP_BASIC; 1.
DR DNA-binding; Hypothetical protein; Nuclear protein.
KW SEQUENCE 454 AA; 49677 MW; B0428D39183374EF CRC64;

Query Match 5.8%; Score 9; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 ALDASLSPV 58
DB 346 ALDASLSPV 354

RESULT 8
O70AKO XENTR PRELIMINARY; PRT; 101 AA.
ID O70AKO_XENTR
AC O70AKO_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibronectin leucine rich transmembrane protein 2 (Fragment).
GN Name=ficr2;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Boettcher R.T., Pollet N., Delius H., Niehrs C.;
RL "The transmembrane protein xFLRT3 forms a complex with FGF receptors
RT and promotes FGF signalling.";
RL Nat. Cell Biol. 6:38-44(2004).
DR EMBL: AJ605779; CAES4089.1; -; mRNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR InterPro: IPR000372; LRK_Nterm.
DR InterPro: IPR001211; PhospholipaseA2.
DR Pfam: PF01462; LRRT; 1.
DR SMART: SM00013; LRRT; 1.
DR PROSITE: PS00119; PA2_ASP; UNKNOWN_1.
KW Transmembrane.
FT NON TER 101
FT SEQUENCE 101 AA; 11296 MW; 27B6A6FC92AE01B1 CRC64;

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Query Match 5.1%; Score 8; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VLYIHHNQ 26
DB 67 VLYIHHNQ 74

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RESULT 9
O70AK1_XENLA PRELIMINARY; PRT: 110 AA.
ID O70AK1_XENLA PRELIMINARY; PRT: 110 AA.
AC O70AK1;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Fibronectin leucine rich transmembrane protein 2 (Fragment).
GN Name=flrt2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
OX NCBI_TaxID=8355;
RA NUCLEOTIDE SEQUENCE.
RP Beutcher R.T., Pollet N., Delius H., Niehrs C.;
RT "The transmembrane protein XFLRT3 forms a complex with FGF receptors
and promotes FGF signalling.";
RL Nat. Cell Biol. 6:38-44(2004).
DR EMBL; AJ605778; CAES408.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000372; IPR_Nterm.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF01462; LRRTNT, 1.
DR SMART; SM00013; LRRTNT, 1.
DR PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
KM Transmembrane.
FT NON TER 110
SQ SEQUENCE 110 AA; 1243 MW; F03922FC059D6F0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 110;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VLYVHNNQ 26
DB 67 VLYVHNNQ 74

RESULT 10
ILIRA_BOVIN STANDARD; PRT: 174 AA.
ID ILIRA_BOVIN STANDARD; PRT: 174 AA.
AC O77482;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IRAP)
DE (IL1 inhibitor) (IL-1RN).
GN Name=IL1RN;
OS Bos taurus (bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
OX NCBI_TaxID=9913;
RA NUCLEOTIDE SEQUENCE.
RP MEDLINE; 96305607; PubMed; 9643454; DOI=10.1016/S0165-2427(98)00099-3;
RX Kitisawa R., Fukuda T., Yamanaka H., Hagiwara K., Goto M., Obata Y.,
RA Yoshino T., Iwai H.;
RA "Enzymatic amplification and expression of bovine interleukin-1
receptor antagonist cDNA.";
RL Vet. Immunol. Immunopathol. 62:197-208(1998).
DE FUNCTION: Inhibits the activity of IL-1 by binding to its
receptor. Has no IL-1 like activity.
DE SUBCELLULAR LOCATION: Secreted.
DE SIMILARITY: Belongs to the IL-1 family.

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removed.

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CC EMBL; AB005148; BAA31854.1; -; mRNA.
DR HSSP; P18510; 11LR.
DR SMR; O77482; 32-174.
DR InterPro; IPR000975; Interleukin_1.
DR InterPro; IPR003297; InterleukinILIRA.
DR PANTHER; PTHR10078:SF2; InterleukinILIRA; 1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PRINTS; PR01360; INTERLEUKIN1X.
DR PRODOM; PD002536; Interleukin_1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 174 Interleukin-1 receptor antagonist
FT CAROHWYD 107 107 protein.
FT DISULFID 89 139 N-linked (GlcNAc..)(Potential).
FT DISULFID 89 139 By similarity.
SQ SEQUENCE 174 AA; 19926 MW; 1B56E7F224F051F CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 1; Length 174;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 118 PGWFLCTS 125
DB 140 PGWFLCTS 147

RESULT 11
Q8Y9D2_LISMO PRELIMINARY; PRT: 196 AA.
ID Q8Y9D2_LISMO PRELIMINARY; PRT: 196 AA.
AC Q8Y9D2;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Lmo0600 protein.
GN OrderedlocusNames=Lmo0600;
DE Lmo0600 protein.
OS Bacteria; Firmicutes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
OX NCBI_TaxID=1639;
RA NUCLEOTIDE SEQUENCE.
RP STRAIN=EGD-e / Serovar 1/2a;
RC MEDLINE; 21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RX Glaeser P., Frangeul L., Buchrieser C., Ruenick C., Amend A.,
RA Baquero F., Berche P., Biocher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Darvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fahi H., Garcia-del Portillo F., Garrido P., Jackson D.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,
RA Madueno E., Matounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RA "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
RA EMBL; AL591976; CAC98678.1; -; Genomic DNA.
DR PIR; AH1149; AH1149.
DR L1etlist; LMO0600; -.
KW Complete proteome.
SQ SEQUENCE 196 AA; 22125 MW; EBB2F568F9C5EBB CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 196;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 LSPVILGV 62
DB 130 LSPVILGV 137

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RESULT 12
Q92E52_LISIN
ID Q92E52_LISIN PRELIMINARY; PRT; 196 AA.
AC Q92E52;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lin0609 protein.
GN OrderedLocustNames=lin0609;
OS Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=1679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Chabdic A., Cheroutant F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Eutian K.-D., Fslhi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Geobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapatk G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng P., Nedjari H.,
RA Nordisk G., Novella S., de Pablos B., Perez-Diaz J.-C., Purrell R.,
RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL, AL596165; CAC95841.1; -; Genomic_DNA.
DR PIR, A11508; A11508.
DR ListerList; LIN0609; -.
KW Complete proteome.
SQ SEQUENCE 196 AA; 22236 MW; 676734063FD3E9E1 CRC64;

Query Match 5.1%; Score 8; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LSPVILGV 62
DB 130 LSPVILGV 137

RESULT 13
Q722V0_LISMF
ID Q722V0_LISMF PRELIMINARY; PRT; 196 AA.
AC Q722V0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=IMOF2365_0629;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Peterson J.F., Raako D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beaman M.J.,
RA Binkac L.M., Daugherty S.C., Dodson R.U., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Tran B., Katharou C.M., Wonderling L.D., Uhlich G.A.,
RA Bayles D.O., Luchansky J.B., Fraser S.C.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen Listeria monocytogenes reveal new insights into the core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
DR EMBL, AB017324; AAT03411.1; -; Genomic_DNA.
DR TIGR, IMOF2365_0629; -.
KW Complete proteome; Hypothetical protein.

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SQ SEQUENCE 196 AA; 22059 MW; 55B5C6BEBBF58A9 CRC64;

Query Match 5.1%; Score 8; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LSPVILGV 62
DB 130 LSPVILGV 137

RESULT 14
Q6E4C0_PETWA
ID Q6E4C0_PETWA PRELIMINARY; PRT; 263 AA.
AC Q6E4C0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Variable lymphocyte receptor.
OS Petromyzon martinus (Sea Lamprey).
OC Petromyzontiformes; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15241406; DOI=10.1038/nature02740;
RA Panzer Z., Amemiya C.T., Enhardt G.R., Cellin J., Larry Gartland G.,
RA Cooper M.D.;
RT "Somatic diversification of variable lymphocyte receptors in the agnathan sea lamprey.";
RL Nature 430:174-180(2004).
DR EMBL, AY578053; AAT70322.1; -; mRNA.
DR EMBL, AY578050; AAT70319.1; -; mRNA.
DR GO, GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF01462; LRRNT_1.
DR Pfam; PF00560; LRR_1; 3.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00013; LRRNT_1.
DR SMART; SM00369; LRR_Typ; 3.
KW Receptor.
SQ SEQUENCE 263 AA; 28326 MW; D53ECBAA7095F73 CRC64;

Query Match 5.1%; Score 8; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 LYLNNOQL 27
DB 102 LYLNNOQL 109

RESULT 15
Q6ETX4_ORYZA
ID Q6ETX4_ORYZA PRELIMINARY; PRT; 278 AA.
AC Q6ETX4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative phospholipidyltransferase isomerase 1 (PAIL1).
GN Name=PO006C08.30;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AP004683; BAD7896.1; -; Genomic_DNA.

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DR Gramene; Q6ETX4; -
 DR GO; GO:0016853; F:isomerase activity; IEA.
 DR GO; GO:0004640; F:phosphoribosylanthranilate isomerase activity; IEA.
 DR GO; GO:0006568; P:Cryptophan metabolism; IEA.
 DR InterPro; IPR001240; PRAI.
 DR Pfam; PF00697; PRAI; 1.
 KW Isomerase.
 SQ SEQUENCE 278 AA; 29698 MW; 9C5D8B8E3720C636 CRC64;

Query Match 5.1%; Score 8; DB 2; Length 278;
 Best Local Similarity 100.0%; Pred.No.16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGGLHA 34
 |||||
 Db 223 LLAGGLHA 230

Search completed: April 5, 2006, 15:14:01
 Job time : 78 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:11:02 ; Search time 19 Seconds
(without alignments)
678.811 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 156
Sequence: 1 MMTLSGALCFRMDKSLAKVL.....IPEDPAMDAPITDTPYFOQCD 156

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 8

Total number of hits satisfying chosen parameters: 40

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/aa/6.COMB.pep:*
3: /cgn2_6/ptodata/1/aa/H.COMB.pep:*
4: /cgn2_6/ptodata/1/aa/PCTUS.COMB.pep:*
5: /cgn2_6/ptodata/1/aa/RE.COMB.pep:*
6: /cgn2_6/ptodata/1/aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156	100.0	156	2	US-09-398-412B-13
2	154	98.7	154	2	US-09-775-046-11
3	44	28.2	80	2	US-09-417-455-3
4	44	28.2	80	2	US-09-348-942-3
5	44	28.2	80	2	US-09-457-626-3
6	44	28.2	80	2	US-09-576-008-3
7	44	28.2	155	2	US-09-417-455-5
8	44	28.2	155	2	US-09-348-942-5
9	44	28.2	155	2	US-09-316-081-5
10	44	28.2	155	2	US-09-578-458-5
11	44	28.2	155	2	US-09-522-964A-5
12	44	28.2	155	2	US-09-457-626-5
13	44	28.2	155	2	US-09-576-008-5
14	44	28.2	155	2	US-09-949-016-6827
15	44	28.2	155	2	US-09-775-046-2
16	44	28.2	187	2	US-09-949-016-9356
17	10	6.4	145	2	US-09-248-796A-25019
18	9	5.8	454	2	US-09-416-050A-6
19	9	5.8	454	2	US-09-664-800-6
20	9	5.8	454	2	US-09-665-309-6
21	9	5.8	454	2	US-09-661-569-6
22	8	5.1	136	2	US-09-647-224A-22
23	8	5.1	268	2	US-09-647-224A-20
24	8	5.1	275	2	US-09-647-224A-24
25	8	5.1	660	2	US-09-907-794A-28
26	8	5.1	660	2	US-09-905-125A-28
27	8	5.1	660	2	US-09-902-775A-28

28	8	5.1	660	2	US-09-906-700-28	Sequence 28, Appl
29	8	5.1	660	2	US-09-903-603A-28	Sequence 28, Appl
30	8	5.1	660	2	US-09-904-920A-28	Sequence 28, Appl
31	8	5.1	660	2	US-09-949-016-6843	Sequence 6843, Ap
32	8	5.1	660	2	US-09-909-064-28	Sequence 28, Appl
33	8	5.1	660	2	US-09-905-061A-28	Sequence 28, Appl
34	8	5.1	660	2	US-09-906-618-28	Sequence 28, Appl
35	8	5.1	660	2	US-09-906-646-28	Sequence 28, Appl
36	8	5.1	660	2	US-09-689-486-58	Sequence 58, Appl
37	8	5.1	660	2	US-09-904-462-28	Sequence 28, Appl
38	8	5.1	660	2	US-09-902-736A-28	Sequence 28, Appl
39	8	5.1	660	2	US-09-906-722A-28	Sequence 28, Appl
40	8	5.1	683	2	US-09-949-016-7267	Sequence 7267, Ap

ALIGNMENTS

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RESULT 1
US-09-398-412B-13
Sequence 13, Application US/09398412B
Patent No. 6680380
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related re
FILE REFERENCE: DX0904K
CURRENT APPLICATION NUMBER: US/09/398, 412B
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: US 60/100948
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 156
TYPE: PRT
ORGANISM: Mus musculus
US-09-398-412B-13

Query Match      100.0%; Score 156; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 6.9e-154;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MMTLSGALCFRMDKSLAKVLYLHNNOLLAGLHAERVIKGEBSIVPNRALDASLSPVIL 60
DB      1 MMTLSGALCFRMDKSLAKVLYLHNNOLLAGLHAERVIKGEBSIVPNRALDASLSPVIL 60

QY      61 GVGGSQCISCGTEKEGPIKLAEPVNIMELYLGAKEKSFYPRDMGLTSSFFSAAYPGW 120
DB      61 GVGGSQCISCGTEKEGPIKLAEPVNIMELYLGAKEKSFYPRDMGLTSSFFSAAYPGW 120

QY      121 FLCTSPADQPVRLTQIPEDPAMDAPITDTPYFOQCD 156
DB      121 FLCTSPADQPVRLTQIPEDPAMDAPITDTPYFOQCD 156

RESULT 2
US-09-775-046-11
Sequence 11, Application US/09775046
Patent No. 6843987
GENERAL INFORMATION:
APPLICANT: Debets, Johannes Eduard Maria Antonius
APPLICANT: Timans, Jacqueline C.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
FILE REFERENCE: DX01073K
CURRENT APPLICATION NUMBER: US/09/775, 046
CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/179, 638
PRIOR FILING DATE: 2000-02-02
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
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/ SEQ ID NO 11
/ LENGTH: 154
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-775-046-11

Query Match      98.7%; Score 154; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.1e-152;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 VTSALCFPMKDSALVLYIHNNQLAGGHAHKVKGSEISVPPRALDASIPVILGV 62
      1 VTSALCFPMKDSALVLYIHNNQLAGGHAHKVKGSEISVPPRALDASIPVILGV 60
      63 QGGSQCLSGCTEGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWFL 122
      61 QGGSQCLSGCTEGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWFL 120
      123 CTSPEADQPVRLTQIPEDPAMDAPITDFYFQOCD 156
      121 CTSPEADQPVRLTQIPEDPAMDAPITDFYFQOCD 154
DB

RESULT 3
US-09-417-455-3
/ Sequence 3, Application US/09417455
/ Patent No. 6294655
/ GENERAL INFORMATION:
/ APPLICANT: Ford, John
/ APPLICANT: Pace, Ann
/ TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
/ FILE REFERENCE: 28110/36328
/ CURRENT APPLICATION NUMBER: US/09/417,455
/ PRIOR FILING DATE: 1999-10-13
/ PRIOR APPLICATION NUMBER: US 09/348,942
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: PCT/US99/04291
/ PRIOR FILING DATE: 1999-04-05
/ PRIOR APPLICATION NUMBER: US 09/287,210
/ PRIOR FILING DATE: 1999-04-05
/ PRIOR APPLICATION NUMBER: US 09/251,370
/ PRIOR FILING DATE: 1999-02-17
/ PRIOR APPLICATION NUMBER: US 09/229,591
/ PRIOR FILING DATE: 1999-01-13
/ PRIOR APPLICATION NUMBER: US 09/127,698
/ PRIOR FILING DATE: 1998-07-31
/ PRIOR APPLICATION NUMBER: US 09/099,818
/ PRIOR FILING DATE: 1998-06-19
/ PRIOR APPLICATION NUMBER: US 09/082,364
/ PRIOR FILING DATE: 1998-05-20
/ PRIOR APPLICATION NUMBER: US 09/079,909
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: US 09/055,010
/ PRIOR FILING DATE: 1998-04-03
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 80
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-417-455-3

Query Match      28.2%; Score 44; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 5.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWFLCT 124
      5 LEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWFLCT 48
DB

RESULT 4
US-09-348-942-3

/ Sequence 3, Application US/09348942
/ Patent No. 6337072
/ GENERAL INFORMATION:
/ APPLICANT: John Ford
/ APPLICANT: Pace, Ann
/ TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
/ FILE REFERENCE: 28110/36010
/ CURRENT APPLICATION NUMBER: US/09/348,942
/ CURRENT FILING DATE: 1999-07-07
/ EARLIER APPLICATION NUMBER: PCT/US99/04291
/ EARLIER FILING DATE: 1999-04-05
/ EARLIER APPLICATION NUMBER: US 09/287,210
/ EARLIER FILING DATE: 1999-04-05
/ EARLIER APPLICATION NUMBER: US 09/251,370
/ EARLIER FILING DATE: 1999-02-17
/ EARLIER APPLICATION NUMBER: US 09/229,591
/ EARLIER FILING DATE: 1999-01-13
/ EARLIER APPLICATION NUMBER: US 09/127,698
/ EARLIER FILING DATE: 1998-07-31
/ EARLIER APPLICATION NUMBER: US 09/099,818
/ EARLIER FILING DATE: 1998-06-19
/ EARLIER APPLICATION NUMBER: US 09/082,364
/ EARLIER FILING DATE: 1998-05-20
/ EARLIER APPLICATION NUMBER: US 09/079,909
/ EARLIER FILING DATE: 1998-05-15
/ EARLIER APPLICATION NUMBER: US 09/055,010
/ EARLIER FILING DATE: 1998-04-03
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 80
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-348-942-3

Query Match      28.2%; Score 44; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 5.9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWFLCT 124
      5 LEPVNIMELYGAKESKSFYRRDMGLTSSFESAAYPGWFLCT 48
DB

RESULT 5
US-09-457-626-3
/ Sequence 3, Application US/09457626
/ Patent No. 6426191
/ GENERAL INFORMATION:
/ APPLICANT: Ford, John
/ APPLICANT: Pace, Ann
/ TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
/ FILE REFERENCE: 28110/36010
/ CURRENT APPLICATION NUMBER: US/09/457,626
/ CURRENT FILING DATE: 1999-12-08
/ EARLIER APPLICATION NUMBER: US 09/417,455
/ EARLIER FILING DATE: 1999-10-13
/ EARLIER APPLICATION NUMBER: US 09/348,942
/ EARLIER FILING DATE: 1999-07-07
/ EARLIER APPLICATION NUMBER: PCT/US99/04291
/ EARLIER FILING DATE: 1999-04-05
/ EARLIER APPLICATION NUMBER: US 09/287,210
/ EARLIER FILING DATE: 1999-04-05
/ EARLIER APPLICATION NUMBER: US 09/229,591
/ EARLIER FILING DATE: 1999-01-13
/ EARLIER APPLICATION NUMBER: US 09/127,698
/ EARLIER FILING DATE: 1998-07-31
/ EARLIER APPLICATION NUMBER: US 09/099,818
/ EARLIER FILING DATE: 1998-06-19
/ EARLIER APPLICATION NUMBER: US 09/082,364
/ EARLIER FILING DATE: 1998-05-20
/ EARLIER APPLICATION NUMBER: US 09/079,909
```

```

; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-626-3

```

```

Query Match      28.2%; Score 44; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 5,9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      81 LEPVIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 124
Db      5 LEPVIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 48

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RESULT 6
US-09-576-008-3
; Sequence 3, Application US/09576008
; Patent No. 6541623
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice Suk-ye
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36456
; CURRENT APPLICATION NUMBER: US/09/576,008
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/523,552
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/457,626
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 09/417,455
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-576-008-3

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```

Query Match      28.2%; Score 44; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 5,9e-38;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      81 LEPVIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 124
Db      5 LEPVIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 48

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RESULT 7
US-09-417-455-5
; Sequence 5, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-417-455-5

```

```

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      81 LEPVIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 124
Db      80 LEPVIMELYGAKESKSFYRRDMGLTSSPESAAYPGWFLCT 123

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RESULT 8
US-09-348-942-5
; Sequence 5, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/35801
; CURRENT APPLICATION NUMBER: US/09/348,942
; CURRENT FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364

```

```

; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatsSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-348-942-5
```

```

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      81 LEPVNIMELYLGAKESKSFYRRDMDGLTSSPESAAYPGWFLCT 124
DB      80 LEPVNIMELYLGAKESKSFYRRDMDGLTSSPESAAYPGWFLCT 123
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RESULT 9
US-09-316-081-5
; Sequence 5, Application US/09316081
; Patent No. 6339141
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/35659
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-316-081-5
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Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY      81 LEPVNIMELYLGAKESKSFYRRDMDGLTSSPESAAYPGWFLCT 124
DB      80 LEPVNIMELYLGAKESKSFYRRDMDGLTSSPESAAYPGWFLCT 123
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RESULT 10
US-09-578-458-5
; Sequence 5, Application US/09578458
; Patent No. 6365726
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice
; APPLICANT: Lin, Hai Shan
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/36479
; CURRENT FILING DATE: US/09/578,458
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/522,964
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/316,086
; PRIOR FILING DATE: 1999-03-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-578-458-5
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Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY      81 LEPVNIMELYLGAKESKSFYRRDMDGLTSSPESAAYPGWFLCT 124
DB      80 LEPVNIMELYLGAKESKSFYRRDMDGLTSSPESAAYPGWFLCT 123
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RESULT 11
US-09-522-964A-5
; Sequence 5, Application US/09522964A
; Patent No. 6372892
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Pace, Ann M.
; APPLICANT: Lin, Hai Shan
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/36210
; CURRENT FILING DATE: US/09/522,964A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/316,086
; PRIOR FILING DATE: 1999-03-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-964A-5
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Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      81 LEPVNIMELYLGAKESKSFYRRDMDGLTSSPESAAYPGWFLCT 124
DB      80 LEPVNIMELYLGAKESKSFYRRDMDGLTSSPESAAYPGWFLCT 123
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RESULT 12
US-09-457-626-5
; Sequence 5, Application US/09457626
; Patent No. 6426191
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36010
; CURRENT FILING DATE: US/09/457,626
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: US 09/417,455
; EARLIER FILING DATE: 1999-10-13
; EARLIER APPLICATION NUMBER: US 09/348,942
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
```



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/ EARLIER FILING DATE: 1998-05-15
/ EARLIER APPLICATION NUMBER: US 09/055,010
/ EARLIER FILING DATE: 1998-04-03
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 5
/ LENGTH: 155
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-457-626-5

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGMFLCT 124
      80 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGMFLCT 123

RESULT 13
US-09-576-008-5
/ Sequence 5, Application US/09576008
/ Patent No. 6541623
/ GENERAL INFORMATION:
/ APPLICANT: Ford, John
/ APPLICANT: Ho, Alice Suk-yue
/ APPLICANT: Pace, Ann
/ TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
/ FILE REFERENCE: 28110/36456
/ CURRENT APPLICATION NUMBER: US/09/576,008
/ CURRENT FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 09/523,552
/ PRIOR FILING DATE: 2000-03-10
/ PRIOR APPLICATION NUMBER: US 09/457,626
/ PRIOR FILING DATE: 1998-12-08
/ PRIOR APPLICATION NUMBER: US 09/417,455
/ PRIOR FILING DATE: 1999-10-13
/ PRIOR APPLICATION NUMBER: US 09/348,942
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: PCT/US99/04291
/ PRIOR FILING DATE: 1999-04-05
/ PRIOR APPLICATION NUMBER: US 09/287,210
/ PRIOR FILING DATE: 1999-04-05
/ PRIOR APPLICATION NUMBER: US 09/251,370
/ PRIOR FILING DATE: 1999-02-17
/ PRIOR APPLICATION NUMBER: US 09/229,591
/ PRIOR FILING DATE: 1998-01-13
/ PRIOR APPLICATION NUMBER: US 09/127,698
/ PRIOR FILING DATE: 1998-07-31
/ PRIOR APPLICATION NUMBER: US 09/099,818
/ PRIOR FILING DATE: 1998-06-19
/ PRIOR APPLICATION NUMBER: US 09/082,364
/ PRIOR FILING DATE: 1998-05-20
/ PRIOR APPLICATION NUMBER: US 09/079,909
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: US 09/055,010
/ PRIOR FILING DATE: 1998-04-03
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 5
/ LENGTH: 155
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-576-008-5

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGMFLCT 124
      80 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGMFLCT 123
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RESULT 14
US-09-949-016-6827
/ Sequence 6827, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6827
/ LENGTH: 155
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-6827

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGMFLCT 124
      80 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGMFLCT 123

RESULT 15
US-09-775-046-2
/ Sequence 2, Application US/09775046
/ Patent No. 6843987
/ GENERAL INFORMATION:
/ APPLICANT: Debets, Johannes Eduard Maria Antonius
/ APPLICANT: Timans, Jacqueline C.
/ APPLICANT: Bazan, J. Fernando
/ APPLICANT: Kaseleijn, Robert A.
/ TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
/ FILE REFERENCE: DX01073X
/ CURRENT APPLICATION NUMBER: US/09/775,046
/ CURRENT FILING DATE: 2001-02-01
/ PRIOR APPLICATION NUMBER: 60/179,638
/ PRIOR FILING DATE: 2000-02-02
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 155
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-775-046-2

Query Match      28.2%; Score 44; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGMFLCT 124
      80 LEPVNIMELYLGAKESKSFYRRDMGLTSSFESAAYPGMFLCT 123

Search completed: April 5, 2006, 15:11:28
Job time : 19 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:11:37 ; Search time 45 Seconds
(without alignments)
1448.475 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 156
Sequence: 1 MMVLGALCFRMKDSALKVL.....IPEDPAWDAPITDFPOCCD 156

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 8

Total number of hits satisfying chosen parameters: 766

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- Published Applications_AA_Main:*
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 - 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
 - 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	156	100.0	156	3	US-09-770-528-2
2	156	100.0	156	3	US-09-965-640-2
3	156	100.0	156	4	US-10-267-791-2
4	156	100.0	156	4	US-10-042-865-124
5	156	100.0	156	4	US-10-695-195-13
6	156	100.0	156	4	US-10-694-978-13
7	156	100.0	156	4	US-10-734-985-2
8	156	100.0	156	5	US-10-948-920-2
9	155	99.4	155	4	US-10-042-865-123
10	154	98.7	154	3	US-09-775-046-11
11	146	93.6	146	3	US-09-730-617-55
12	80	28.2	80	4	US-10-205-821-7
13	143	28.2	143	4	US-10-287-190-70
14	143	28.2	143	4	US-10-287-190-76
15	144	28.2	143	4	US-10-287-190-75
16	144	28.2	146	3	US-09-730-617-58
17	144	28.2	147	3	US-09-730-617-76
18	147	28.2	147	4	US-10-205-821-7
19	155	28.2	155	3	US-09-730-617-61
20	155	28.2	155	3	US-09-730-617-80
21	155	28.2	155	3	US-09-730-617-96
22	155	28.2	155	3	US-09-775-046-2
23	155	28.2	155	3	US-09-965-640-4
24	155	28.2	155	4	US-10-006-867-152
25	155	28.2	155	4	US-10-003-671A-5
26	155	28.2	155	4	US-10-063-547-152
27	155	28.2	155	4	US-10-063-551-152

28	155	4	US-10-139-833-10	Sequence 10, App1
29	155	4	US-10-063-616-152	Sequence 152, App
30	155	4	US-10-063-569-152	Sequence 152, App
31	155	4	US-10-063-513-152	Sequence 152, App
32	155	4	US-10-063-515-152	Sequence 152, App
33	155	4	US-10-063-512-152	Sequence 152, App
34	155	4	US-10-063-502-152	Sequence 152, App
35	155	4	US-10-063-549-152	Sequence 152, App
36	155	4	US-10-063-554-152	Sequence 152, App
37	155	4	US-10-063-553-152	Sequence 152, App
38	155	4	US-10-063-518-152	Sequence 152, App
39	155	4	US-10-063-598-152	Sequence 152, App
40	155	4	US-10-227-693-152	Sequence 152, App
41	155	4	US-10-267-791-5	Sequence 5, App1
42	155	4	US-10-063-563-152	Sequence 152, App
43	155	4	US-10-063-555-152	Sequence 152, App
44	155	4	US-10-063-594-152	Sequence 152, App
45	155	4	US-10-063-567-152	Sequence 152, App

ALIGNMENTS

RESULT 1
US-09-770-528-2
Sequence 2, Application US/09770528
Patent No. US20020164332A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Sana, Theodore R.
Bazan, Fernando J.
Kastelein, Robert A.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,528
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/130,972
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/055,111
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: US 09/062,866
FILING DATE: 20-APR-1998
APPLICATION NUMBER: US 09/097,976
FILING DATE: 16-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0725X2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
FAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-770-528-2

Query Match 100.0%; Score 156; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVKIKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVKIKGEISVVPNRALDASISPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEBPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEBPAMDAPITDFYFOQCD 156

RESULT 2

US-09-965-640-2
Sequence 2, Application US/09965640
Publication No. US20020187122A1
GENERAL INFORMATION:
APPLICANT: Sims, John E.
TITLE OF INVENTION: IL-1 DELTA DNA AND POLYPEPTIDES
FILE REFERENCE: 0315-C
CURRENT APPLICATION NUMBER: US/09/965,640
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/612,921
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 156
TYPE: PRT
ORGANISM: Mus musculus
US-09-965-640-2

Query Match 100.0%; Score 156; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVKIKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVKIKGEISVVPNRALDASISPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEBPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEBPAMDAPITDFYFOQCD 156

RESULT 3

US-10-267-791-2
Sequence 2, Application US/10267791
Publication No. US20030059892A1
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF THE TANGO-93-RELATED PROTEIN FAMILY
FILE REFERENCE: 07334-200001 (formerly 09404/086001)
CURRENT APPLICATION NUMBER: US/10/267,791
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/369,693
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: US 09/331,263
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 156
TYPE: PRT
ORGANISM: Mus musculus
US-10-267-791-2

Query Match 100.0%; Score 156; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVKIKGEISVVPNRALDASISPVIL 60
DB 1 MMVLSGALCFRMDKSAIKVLYLHNNQLAGLHAKEVKIKGEISVVPNRALDASISPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGW 120
QY 121 FLCTSPBADQPVRLTQIPEBPAMDAPITDFYFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEBPAMDAPITDFYFOQCD 156

RESULT 4

US-10-042-865-124
Sequence 124, Application US/10042865
Publication No. US20040029216A1
GENERAL INFORMATION:
APPLICANT: Padigar, Muralidhara
APPLICANT: Li, Li
APPLICANT: Zernusen, Bryan D
APPLICANT: Caeman, Steacie J
APPLICANT: Shenoy, Sureesh G
APPLICANT: Spytek, Kimberly
APPLICANT: Zhong, Mei
APPLICANT: Gangoli, Beha A
APPLICANT: Burgess, Catherine B
APPLICANT: Paturajan, Meera
APPLICANT: Verne, Corine A.M
APPLICANT: Taylor, Sarah
APPLICANT: Tcherev, Velizar T
APPLICANT: Miller, Charles E
APPLICANT: Guo, Xiaojia
APPLICANT: Boldog, Ference L
APPLICANT: Grose, William M
APPLICANT: Alsbrook II, John P
APPLICANT: Gerlach, Valerie L
APPLICANT: Edinger, Shlomit R
APPLICANT: Rothenberg, Mark E
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Malyankar, Uriel M
APPLICANT: Miller, Isabelle
APPLICANT: Peyman, John
APPLICANT: Smithson, Glennda
APPLICANT: Gunther, Erik
APPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: US/10/042,865
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/272,338
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR FILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 264
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 124
LENGTH: 156
TYPE: PRT
ORGANISM: Mus. musculus
US-10-042-865-124

Query Match 100.0%; Score 156; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGLHAERKVIKGEETISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGLHAERKVIKGEETISVVPNRALDASLSPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAVPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAVPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOQCD 156

RESULT 5

US-10-695-195-13
Sequence 13, Application US/10695195
Publication No. US20040068099A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/695,195
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-695-195-13

Query Match 100.0%; Score 156; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGLHAERKVIKGEETISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGLHAERKVIKGEETISVVPNRALDASLSPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAVPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAVPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOQCD 156

RESULT 6

US-10-694-978-13
Sequence 13, Application US/10694978
Publication No. US2004008766A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/694,978
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-694-978-13

Query Match 100.0%; Score 156; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGLHAERKVIKGEETISVVPNRALDASLSPVIL 60
DB 1 MMVLSGALCFRMDKSAKLVLYLHNNQLAGLHAERKVIKGEETISVVPNRALDASLSPVIL 60
QY 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAVPGW 120
DB 61 GVQGSQCLSCGTEKGPILKLEPVNIMELYGAKESKSFYRRDMGLTSSPESAAVPGW 120
QY 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOQCD 156
DB 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFFFOQCD 156

RESULT 7

US-10-734-985-2
; Sequence 2, Application US/10734985
; Publication No. US20040142420A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TANGO-93-RELATED
; FILE REFERENCE: 07334-369001
; CURRENT FILING DATE: 2003-12-12
; PRIOR FILING DATE: 2002-04-29
; PRIOR FILING DATE: 2002-04-29
; PRIOR FILING DATE: 1998-08-07
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-734-985-2

Query Match 100.0%; Score 156; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMTLSGALCFRMKDSALKVLTLHNNQLLAGGHAKEVIGKEEISVVPNRALDASISPVYL 60
Db 1 MMTLSGALCFRMKDSALKVLTLHNNQLLAGGHAKEVIGKEEISVVPNRALDASISPVYL 60
Qy 61 GVGGSGQLSCGTEKGPILKEPVNIMELYGAKSKSFYFRDMGLTSSPESAAYPGW 120
Db 61 GVGGSGQLSCGTEKGPILKEPVNIMELYGAKSKSFYFRDMGLTSSPESAAYPGW 120
Qy 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
Db 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 8

US-10-948-920-2
; Sequence 2, Application US/10948920
; Publication No. US20050058625A1
; GENERAL INFORMATION:
; APPLICANT: Sime, John E.
; TITLE OF INVENTION: IL-1 DELTA DNA AND POLYPEPTIDES
; FILE REFERENCE: 0315-C
; CURRENT FILING DATE: 2004-09-23
; PRIOR FILING DATE: 2004-09-23
; PRIOR FILING DATE: 2001-09-27
; PRIOR FILING DATE: 2001-09-27
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-948-920-2

Query Match 100.0%; Score 156; DB 5; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.4e-145;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMTLSGALCFRMKDSALKVLTLHNNQLLAGGHAKEVIGKEEISVVPNRALDASISPVYL 60
Db 1 MMTLSGALCFRMKDSALKVLTLHNNQLLAGGHAKEVIGKEEISVVPNRALDASISPVYL 60

Qy 61 GVGGSGQLSCGTEKGPILKEPVNIMELYGAKSKSFYFRDMGLTSSPESAAYPGW 120
Db 61 GVGGSGQLSCGTEKGPILKEPVNIMELYGAKSKSFYFRDMGLTSSPESAAYPGW 120
Qy 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156
Db 121 FLCTSPBADQPVRLTQIPEDPAMDAPITDFYFOQCD 156

RESULT 9

US-10-042-865-123
; Sequence 123, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: zerhusen, Bryan D
; APPLICANT: Caeman, Stacie J
; APPLICANT: Shenoy, Sureeh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangoli, Neha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Paturajan, Meera
; APPLICANT: Verneet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Renese L
; APPLICANT: Groese, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellemann, Karen
; APPLICANT: Macdougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT FILING DATE: 2002-05-17
; PRIOR FILING DATE: 2002-05-17
; PRIOR FILING DATE: 2001-01-09
; PRIOR FILING DATE: 2001-01-09
; PRIOR FILING DATE: 2001-01-10
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2001-03-09
; PRIOR FILING DATE: 2001-03-09
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-042-865-123

Query Match 99.4%; Score 155; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.2e-144;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MMTLSGALCFRMKDSALKVLTLHNNQLLAGGHAKEVIGKEEISVVPNRALDASISPVILG 61
Db 1 MMTLSGALCFRMKDSALKVLTLHNNQLLAGGHAKEVIGKEEISVVPNRALDASISPVILG 60

QY 62 VGGSSQCLSCCTEKGPIIKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 121
DB 61 VGGSSQCLSCCTEKGPIIKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 120
QY 122 LCTSPADQPVRLTQIPEDPAMDAPITDFFYQOCD 156
DB 121 LCTSPADQPVRLTQIPEDPAMDAPITDFFYQOCD 155

RESULT 10
US-09-775-046-11
; Sequence 11, Application US/09775046
; Patent No. US20020102234A1
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/775,046
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-775-046-11

Query Match 98.7%; Score 154; DB 3; Length 154;
Best Local Similarity 100.0%; Pred. No. 5e-143;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLSGALCFRMDKALKLYLHNNQLAGLHAKEVITGEBISVVPNRALDASLSPVILGV 62
DB 1 VLSGALCFRMDKALKLYLHNNQLAGLHAKEVITGEBISVVPNRALDASLSPVILGV 60
QY 63 QGSSQCLSCCTEKGPIIKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 122
DB 61 QGSSQCLSCCTEKGPIIKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWF 120
QY 123 CTSPEADQPVRLTQIPEDPAMDAPITDFFYQOCD 156
DB 121 CTSPEADQPVRLTQIPEDPAMDAPITDFFYQOCD 154

RESULT 11
US-09-730-617-55
; Sequence 55, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhidas K
; APPLICANT: Shinketsu, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zethusen, Bryan D
; APPLICANT: Mezei, Peter S
; TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 55
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-617-55

Query Match 93.6%; Score 146; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.5e-135;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CFRMDKALKLYLHNNQLAGLHAKEVITGEBISVVPNRALDASLSPVILGVGGSSQC 68
DB 1 CFRMDKALKLYLHNNQLAGLHAKEVITGEBISVVPNRALDASLSPVILGVGGSSQC 60
QY 69 LSCGTEKGPIIKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWFLCTSPEA 128
DB 61 LSCGTEKGPIIKLEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWFLCTSPEA 120
QY 129 DQPVRLTQIPEDPAMDAPITDFFYQO 154
DB 121 DQPVRLTQIPEDPAMDAPITDFFYQO 146

RESULT 12
US-10-205-821-1
; Sequence 1, Application US/10205821
; Publication No. US20030099650A1
; GENERAL INFORMATION:
; APPLICANT: Ho et al.
; TITLE OF INVENTION: Treatment of Immune Disorders and B Cell Disorders
; FILE REFERENCE: 28110/78645
; CURRENT APPLICATION NUMBER: US/10/205,821
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-821-1

Query Match 28.2%; Score 44; DB 4; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 LEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWFLCT 124
DB 5 LEPVNIMELYLGAKESKSFYFRDMGLTSSFESAAYPGWFLCT 48
RESULT 13
US-10-287-190-70
; Sequence 70, Application US/10287190
; Publication No. US20040038230A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P. et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND MET
; FILE REFERENCE: 21402-780B
; CURRENT APPLICATION NUMBER: US/10/287,190
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 09/996,015
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/338626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/373806
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/338196
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/333912

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/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 60/381043
/ PRIOR FILING DATE: 2002-05-16
/ PRIOR APPLICATION NUMBER: 60/401593
/ PRIOR FILING DATE: 2002-08-07
/ PRIOR APPLICATION NUMBER: 60/334300
/ PRIOR FILING DATE: 2001-11-29
/ NUMBER OF SEQ ID NOS: 194
/ SOFTWARE: CuraSeqList version 0.1
/ SEQ ID NO: 70
/ LENGTH: 143
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-287-190-70
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```
Query Match      28.2% Score 44; DB 4; Length 143;
Best Local Similarity 100.0%; Pred.No. 6.7e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      81 LEPVNIMELYLGAKESKSFIFYRDMGLTSSPESAAYPGWFLCT 124
      |||
DB      75 LEPVNIMELYLGAKESKSFIFYRDMGLTSSPESAAYPGWFLCT 118
```

```
RESULT 14
US-10-287-190-76
/ Sequence 76, Application US/10287190
/ Publication No. US20040038230A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsbodtrock II, John P. et al.
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-780B
/ CURRENT APPLICATION NUMBER: US/10/287,190
/ PRIOR FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 09/996,015
/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 60/338626
/ PRIOR FILING DATE: 2001-11-05
/ PRIOR APPLICATION NUMBER: 60/373806
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: 60/338196
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/333912
/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 60/381043
/ PRIOR FILING DATE: 2002-05-16
/ PRIOR APPLICATION NUMBER: 60/401593
/ PRIOR FILING DATE: 2002-08-07
/ PRIOR APPLICATION NUMBER: 60/334300
/ PRIOR FILING DATE: 2001-11-29
/ NUMBER OF SEQ ID NOS: 194
/ SOFTWARE: CuraSeqList version 0.1
/ SEQ ID NO: 76
/ LENGTH: 143
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-287-190-76
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```
Query Match      28.2% Score 44; DB 4; Length 143;
Best Local Similarity 100.0%; Pred.No. 6.7e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      81 LEPVNIMELYLGAKESKSFIFYRDMGLTSSPESAAYPGWFLCT 124
      |||
DB      75 LEPVNIMELYLGAKESKSFIFYRDMGLTSSPESAAYPGWFLCT 118
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```
RESULT 15
US-09-730-617-58
/ Sequence 58, Application US/09730617
/ Patent No. US20020068279A1
/ GENERAL INFORMATION:
/ APPLICANT: Burgees, Catherine E
```

```
/ APPLICANT: Prayaga, Sudhirdas K
/ APPLICANT: Shinkels, Richard A
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Zernusen, Bryan D
/ APPLICANT: Mezes, Peter S
/ TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the S
/ FILE REFERENCE: 15966-609
/ CURRENT APPLICATION NUMBER: US/09/730,617
/ PRIOR FILING DATE: 2000-12-05
/ PRIOR APPLICATION NUMBER: 60/169,056
/ PRIOR FILING DATE: 1999-12-06
/ PRIOR APPLICATION NUMBER: 60/169,886
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 60/169,866
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 60/170,252
/ PRIOR FILING DATE: 1999-12-10
/ PRIOR APPLICATION NUMBER: 60/175,740
/ PRIOR FILING DATE: 2000-01-12
/ NUMBER OF SEQ ID NOS: 100
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 58
/ LENGTH: 146
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-730-617-58
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Query Match      28.2% Score 44; DB 3; Length 146;
Best Local Similarity 100.0%; Pred.No. 6.9e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      81 LEPVNIMELYLGAKESKSFIFYRDMGLTSSPESAAYPGWFLCT 124
      |||
DB      73 LEPVNIMELYLGAKESKSFIFYRDMGLTSSPESAAYPGWFLCT 116
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Search completed: April 5, 2006, 15:12:30
Job time : 45 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 5, 2006, 15:12:38 ; Search time 12 Seconds
(without alignments)
405.496 Million cell updates/sec

Title: US-09-770-528-2

Perfect score: 156
Sequence: 1 MMTLSGALCFRMDKSAKVL.....IPEDPANDAPITDTPFOCCD 156

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 184161 seqs, 31191982 residues

Word size : 8

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.dep.*
- 2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.dep.*
- 3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.dep.*
- 4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.dep.*
- 5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.dep.*
- 6: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.dep.*
- 7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.dep.*
- 8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.dep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	28.2	155	6	US-10-063-703-152
2	44	28.2	155	7	US-11-102-240-152
3	44	28.2	155	7	US-11-103-195-152
4	9	5.8	454	7	US-11-169-013-1
5	8	5.1	206	7	US-11-096-568A-11327
6	8	5.1	234	7	US-11-096-568A-11757
7	8	5.1	262	7	US-11-096-568A-11756
8	8	5.1	264	7	US-11-096-568A-11326
9	8	5.1	308	7	US-11-096-568A-11755
10	8	5.1	335	7	US-11-096-568A-11325
11	8	5.1	660	6	US-10-131-826A-350
12	8	5.1	660	6	US-10-973-115B-350

ALIGNMENTS

RESULT 1
US-10-063-703-152
; Sequence 152, Application US/10063703
; Publication No. US2006008901A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,703
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 152
LENGTH: 155
TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-703-152

Query Match 28.2%; Score 44; DB 6; Length 155;
Best Local Similarity 100.0%; Pred. No. 7.6e-40;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 LEPVIMELYLGAKESSFTFYRDDGLTSSPESAAYPGWFLCT 124
DB 80 LEPVIMELYLGAKESSFTFYRDDGLTSSPESAAYPGWFLCT 123

RESULT 2

US-11-102-240-152
; Sequence 152, Application US/11102240
; Publication No. US20050260647A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPR
FILE OF INVENTION: ESCOPHAGEAL TUMOR
FILE REFERENCE: P3230R1C106C
CURRENT APPLICATION NUMBER: US/11/102,240
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 10/063662
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 199-12-09
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 152
LENGTH: 155
TYPE: PRT
ORGANISM: Homo Sapien
US-11-102-240-152

Query Match 28.2%; Score 44; DB 7; Length 155;
Best Local Similarity 100.0%; Pred. No. 7.6e-40;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 LEPVIMELYLGAKESSFTFYRDDGLTSSPESAAYPGWFLCT 124
DB 80 LEPVIMELYLGAKESSFTFYRDDGLTSSPESAAYPGWFLCT 123

RESULT 3
US-11-103-195-152
; Sequence 152, Application US/11103195
; Publication No. US20060051779A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey


```

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guirey, Auecia L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230C166C1
; CURRENT APPLICATION NUMBER: US/11/103,195
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: 10/063743
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 152
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-103-195-152

Query Match          28.2%; Score 44; DB 7; Length 155;
Best Local Similarity 100.0%; Pred. No. 7,6e-40;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 LEPVNIMELYLGAKESKSFYFRDNGLTSSPESAAYPGMPFLCT 124
DB 80 LEPVNIMELYLGAKESKSFYFRDNGLTSSPESAAYPGMPFLCT 123

RESULT 4
US-11-169-013-1
; Sequence 1, Application US/11169013
; Publication No. US20050244971A1
; GENERAL INFORMATION:
; APPLICANT: Korea Kumho Petrochemical Co., Ltd.
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH ENHANCED STRESS TOLERANCE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/169,013
; CURRENT FILING DATE: 2005-06-29
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Kopatentm 1.71
; SEQ ID NO 1
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-169-013-1

Query Match          5.8%; Score 9; DB 7; Length 454;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 ALDASLSPV 58
DB 346 ALDASLSPV 354

RESULT 5
US-11-096-568A-11327
; Sequence 11327, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01

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; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11327
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(206)
; OTHER INFORMATION: Ceres Seq. ID no. 13598556
US-11-096-568A-11327

Query Match          5.1%; Score 8; DB 7; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGGLHA 34
DB 152 LLAGGLHA 159

RESULT 6
US-11-096-568A-17757
; Sequence 17757, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17757
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(234)
; OTHER INFORMATION: Ceres Seq. ID no. 12360574
US-11-096-568A-17757

Query Match          5.1%; Score 8; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGGLHA 34
DB 180 LLAGGLHA 187

RESULT 7
US-11-096-568A-17756
; Sequence 17756, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17756
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(262)
; OTHER INFORMATION: Ceres Seq. ID no. 12360573
US-11-096-568A-17756

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Query Match 5.1%; Score 8; DB 7; Length 262;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGLHA 34
|||||||
Db 208 LLAGLHA 215

RESULT 8

US-11-096-568A-11326
; Sequence 11326, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theryby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11326
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(264)
; OTHER INFORMATION: Ceres Seq. ID no. 13598555
US-11-096-568A-11326

Query Match 5.1%; Score 8; DB 7; Length 264;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGLHA 34
|||||||
Db 210 LLAGLHA 217

RESULT 9

US-11-096-568A-17755
; Sequence 17755, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theryby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17755
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(308)
; OTHER INFORMATION: Ceres Seq. ID no. 12360572
US-11-096-568A-17755

Query Match 5.1%; Score 8; DB 7; Length 308;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGLHA 34
|||||||
Db 254 LLAGLHA 261

RESULT 10
US-11-096-568A-11325

; Sequence 11325, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theryby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11325
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(335)
; OTHER INFORMATION: Ceres Seq. ID no. 13598554
US-11-096-568A-11325

Query Match 5.1%; Score 8; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LLAGLHA 34
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Db 281 LLAGLHA 288

RESULT 11
US-10-131-826A-350
; Sequence 350, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352

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; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 350
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-350

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Query Match          5.1%; Score 8; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      19 VLYLHNNQ 26
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Db       67 VLYLHNNQ 74

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RESULT 12
US-10-973-115B-350
; Sequence 350, Application US/10973115B
; Publication No. US20060040351A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Quiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODIN
; FILE REFERENCE: 39870-3330R1C300C1
; CURRENT APPLICATION NUMBER: US/10/973,115B
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 10/145,747
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 350
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-115B-350

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Query Match          5.1%; Score 8; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      19 VLYLHNNQ 26

```

```

Db       67 VLYLHNNQ 74
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Search completed: April 5, 2006, 15:12:57
Job time : 13 secs

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